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ANTER-SPECIFIC PROLINE
MAJOR EXTRACELLULAR EN
ANTER-SPECIFIC PROLINE
CAPSID PROTEIN P40 (CO
SINC FINGER PROTEIN HR
HYPOTHETICAL BREF4 PRO
HYPOTHETICAL 29.3 KD P
                                                                                                                                                                        CCAAT/ENHANCER BINDING
HYPOTHETICAL 31.3 KD P
HYPOTHETICAL 37.0 KD P
SPLICEDSOME ASSOCIATED
MOBILIZATION PROTEIN M
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PLATELET GLYCOPROTEIN
ALPHA-L-ARABINOFURANOS
LARGE PROLINE-RICH PRO
HYPOTHETICAL 12.3 KD P
CCAAT/ENHANCER BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MICROSPORE-SPECIFIC PR
HYPOTHETICAL 27.0 KD P
REGULATORY FACTOR X-AS
EARLY EIA 32 KD PROTEI
GLUTBRIN, LOW MOLECULA
GAG POLYPROTEIN (CONTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GLYCOPROTEIN I.
GAG POLYPROTEIN (CONTA
EBNA-2 NUCLEAR PROTEIN
PROSTAGLANDIN G/H SYNT
EXTRACELLULAR SIGNAL-R
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ENDOGLUCANASE A PRECUR
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DNAJ-LIKE PROTEIN MG20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FOS-RELATED ANTIGEN 2.
HYPOTHETICAL 35.5 KD P
1D-MYO-INOSITOL-TRISPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATROPHIN-1 (DENTATORUB
PROTEASE (EC 3.4.23..)
SURVIVAL MOTOR NEURON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROCOLLAGEN ALPHA 1(II
NON-STRUCTURAL POLYPRO
DYNEIN HEAVY CHAIN, CY
CAMPATH-1 ANTIGEN PREC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DESMOCOLLIN 1A/1B PREC
BRIDE OF SEVENLESS PRO
TRANS-ACTING TRANSCRIP
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PROTEIN DISULFIDE ISOM
TRANSCRIPTION ACTIVATO
NITRATE REDUCTASE (EC
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FOS-RELATED ANTIQUEN 2.
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ABFA_STRLI
BATZ_THIFE
CCEBD_HUMAN
VIEN_NPVAC
DUNY_MYCPN
LIO_DROME
LHRN_ECOLI
FRAZ_HUMAN
TY3_STRFR
IP3K_RAT
VL96_IRV1
DRPL_FRAZ_HUMAN
SMNI_HUMAN
PRZ_HTLV2
SMNI_HUMAN
VVEI_HTLV2
VVEI_HTLV3

CDNC_HUMAN
APG_BRANA
GUNA_ZANCP
APG_ARATH
APG_ARATH
HRX_MOUSE
YRR4_EBV
Y091_NPVOP
NUOPP_MOUSE
CEBD_MOUSE
Y114_YEBAT
Y08N_MYCTU
SAX1_CHICK
CEBD_MOUSE
Y114_YEBAT
Y08N_MYCTU
SYL_CHICK
ETBL_HUMAN
MBEA_ECOLI
EXTN_TOBAC
DIK_MOUSE
Y114_YEBAT
Y08N_MYCTU
SYL_CHICK
EXTN_TOBAC
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E1A_ADE02
GLTC_WHEAT
GAG_FSVHZ
VCOM_ADECC
WNTG_DROME
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BRLI_EBV
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DSC1_MOUSE
BOSS_DROME
ICP4_HSV11
CA12_MOUSE
POLN_HEVBU
DYHC_EMENI
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(1-156) from USO8799910.pep
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RADIATION-INDUCIBLE IM 3
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PROBABLE E4 PROTEIN.
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                                                                                                                                                                                                 Release 3.1A John F. Collins, Biocomputing Research Copyright (c) 1993-1998, University of Edinburgh, U. Distribution rights by Oxford Molecular Ltd
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CHS2_PARBR
V120_EBV
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TRANSCRIPTION FACTOR H 4.44e+01 HYPOTHETICAL 31.9 KD P 4.44e+01 VIRAL PROTEIN TPX. 1MYC PROTO-ONCOGENE P 4.44e+01 CYTOCHROME B (EC 1.10. 4.44e+01 CYTOCHROME B (EC 1.10. 4.44e+01 DIHYDROLIPOAMIDE SUCCI 4.44e+01 CARBAMOYL-PHOSPHATE SY 4.44e+01 MINOR CAPSID PROTEIN L 4.44e+01 GLYCOPROTEIN E PRECURS 4.44e+01 CAPSID PROTEIN P40 (CO 4.44e+01 HYPOTHETICAL GREE 28 P 4.44e+01 CAPSID PROTEIN 37,5'-C 4.44e+01 TOPOISOMERASE II-ASSOC 4.44e+01	2A PROTEIN (PROBABLE R 4 44e+01 CYTOKINE RECEPTOR COMM 4.44e+01 IMMEDIATE-EARLY PROTEI 4.44e+01 IMMEDIATE-EARLY PROTEI 4.44e+01 SERINE/THREONINE PROTE 4.44e+01 TRANS-ACTING TRANSCRIP 4.44e+01 TRANS-ACTING TRANSCRIP 4.44e+01 TRANS-ACTING TRANSCRIP 4.44e+01 TRANS-ACTING TRANSCRIP 4.44e+01 ADDENYLATE CYCLASE (EC 4.44e+01 DYNEIN HEAVY CHAIN, CY 4.44e+01 HOMEOBOX PROTEIN CDX-1 5.67e+01 EARLY EIA 32 KD PROTEI 5.67e+01	56 AA. DATE) BEDATE) RE IEX-1 (IMMEDIATE EARLY ROTEIN). FA; TETRAPODA; MAMMALIA;	M.O.; ., KALTHOFF H., FOELSCH U.R.,	SEQUENCE FROM N.A. MEDDINE; 9733426. PIETZSCH A., BUECHLER C., ASLANIDIS C., SCHMITZ G.; BIOCHEM. BIOPHYS. RES. COMMUN. 235:4-9(1997). [4] [4] PRELIMINARY SEQUENCE OF 1-106 FROM N.A. TISSUB-PLACENTA; HILLIER L., CLARK N., DUBUQUE T., ELLISTON K., HAMKINS M., HOLMAN M., HULTMAN M., KUCABA T., LE M., LENNON G., MARRA M., PARSONS J., RIFKIN L., ROHLENG T., TAN F., TREVASKIS E., WATERSTON R., WILLIAMSON A., WOHLDMANN P., WILSON R., SUBMITTED (FEB-1995) TO EMBL/GENBANK/DBJ DATA BANKS. 1- SUBGELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (POTENTIAL). 1- INDUCTION: BY RADIATION, TPA, OKADAIC ACID AND TNF-ALPHA.
HESI_MOUSE YEK2_YERST CCPA_ACEXI VTPX_TTV1 WYCL_MOUSE WYCL_MOUSE CYBA_STELO VE2_HEYT CARA_MEDCR VL2_HEYS VL2_HEYS VL2_HEYS VL2_HEYS VL2_HEYS VGIE_HSYS VGIE VGIE_HSYS VGIE VGIE	1 V2A_CWYO 1 V2A_CWYO 2 VYB_MOUSE 1 DRPL_HUMAN 1 E18_PRVKA 1 DPOA_MOUSE 1 DCA_HSVER 1 ICP4_HSVER 1 CFA_HSVER 1 DYHC_NEUCR 1 CDX1_MOUSE 1 E1A_ADE05	ALIGNMENTS TO; PRT; 15 CREATED) LAST SEQUENCE UPI LAST SEQUENCE UPI LAST ANNOFATION (MCEDIATE - EARLY GER PROTEIN) (DIF-2 PI HORDATA; VERTEBRAI	N.A. 295. 1295. 1498-1502(1996). N.A. RAUZOLD A., LETTAU P., KA	C., ASLANIDIS C., COMMUN. 235:4-99 DF 1-106 FROM N.A. DUBUGUE T., ELLIF LEM., LENNOS, TAN F., TREVASS NNN P., WILSON R.; TO EMBL/GENBANK/DI ON: TYPE II MEMBL INTION, TPPE II MEMBL
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Release 3.1A John F. Collins, Bic Copyright (c) 1993-1998, Universi Distribution rights by On MPSrch_pp protein - protein database sean Run on: Thu Jan 7 11:05:22 1999;	Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998, University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd srch_pp protein - protein database search, using Smith-Waterman algorithm n on: Thu Jan 7 11:05:22 1999; MasPar time 7.06 Seconds 592.942 Million cell updates/sec
	rtabase search, using Smith-Waterman algorithm 15:22 1999; MasPar time 7.06 Seconds 592.942 Million cell updates/sec
r output not generated.	
Title: >US-08-799-910-10 Description: (1-156) from US08799910.pep Perfect Score: 1114 Sequence: 1 MCHSRSCHPTWILLQAPTPA	10 :08799910.pep :LOAPTPAEPSDYALDLSTFLQQHPAAF 156
Scoring table: PAM 150 Gap 11	
Searched: 74019 segs, 26840295 residues	40295 residues
Post-processing: Minimum Match 0% Listing first 200 summaries	00 summaries
Database: swiss-prot35	
Statistics: Mean 44.450; Ve	Mean 44.450; Variance 91.313; scale 0.487

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+[1156		* C			SUMMARIES			
20	Score	Match	Length	DB	ID	Description	Pred. No.	
•	1114	100.0	156	٦	IEX1_HUMAN	RADIATION-INDUCIBLE IM	3.79e-194	
~	752	67.5	153	٦	IEX1_MOUSE	RADIATION-INDUCIBLE IM	3.93e-121	
m	117	10.5	474	٦	VTP3_TTV1V	VIRAL PROTEIN TPX.	2.12e-03	
4	112	10.1	228	٦	VCOM_ADEM1	MINOR CORE PROTEIN (PR	1.01e-02	
'n	109	8.6		Н	YO25_CAEEL	HYPOTHETICAL 202.6 KD	2.51e-02	
Q	103	9.5		-1	FOR4_MOUSE	FORMIN 4 (LIMB DEFORMI	1.50e-01	
7	103	9.5	_	ч	FORM_MOUSE	FORMIN (LIMB DEFORMITY	1.50e-01	
ထ	101	9.1		Н	CEBD_RAT	CCAAT/ENHANCER BINDING	2.68e-01	
σ	101	9.1		Н	A1AB_CANFA	ALPHA-1B ADRENERGIC RE	2.68e-01	
10	101	9.1	816	Н	OA1F_NEUCR	QUINIC ACID UTILIZATIO	2.68e-01	
1	66	8.9	272	~	GSPC_ERWCH	GENERAL SECRETION PATH	4.76e-01	
15	86	8.8	272	7	GSQC_ERWCH	GENERAL SECRETION PATH	6.33e-01	
13	86	8.8	390	Н	VGLI_HSV11	GLYCOPROTEIN I.	6.33e-01	
14	96	8.8	475	٢	GAPN_STRMU	NADP-DEPENDENT GLYCERA	6.33e-01	
15	86	89	519	٦	A1AB_HUMAN	ALPHA-1B ADRENERGIC RE	6.33e-01	
16	98	80.	975	Ч	CDP_CANFA	CCAAT DISPLACEMENT PRO	6.33e-01	
17	97	8.7	1043	-	CHS2_PARBR	CHITIN SYNTHASE 2 (EC	8.39e-01	
18	97	8.7	1239	Н	V120_EBV	CAPSID ASSEMBLY PROTEI	8.39e-01	
19	97	8.7	1337	-1	PTPJ_HUMAN	PROTEIN-TYROSINE PHOSP	8.39e-01	
20	96	8.6	245	Н	VE4_HPV5B	PROBABLE E4 PROTEIN.	1.11e+00	
21	96	8.6	245	ч	VE4_HPV05	PROBABLE E4 PROTEIN.	1.11e+00	
22	96	8.6	1233	-	NME3_HUMAN	GLUTAMATE (NMDA) RECEP	1.11e+00	
23	95	8.5	234	~	GLNA_DUNSA	GLUTAMINE SYNTHETASE (	1.47e+00	

11.47e+00 11.47e+00 11.47e+00 11.47e+00 11.93e+00 11.93e+00 11.93e+00 11.93e+00 12.54e+00 13.34e+00 13.34e+00 13.34e+00 13.34e+00 13.34e+00 13.34e+00 13.34e+00 13.34e+00 13.34e+00 13.34e+00 13.34e+00 13.34e+00 13.34e+00 13.34e+00 13.34e+00 13.34e+00 13.34e+00 13.34e+00 13.34e+00 13.34e+00 13.34e+00 13.34e+00 13.34e+00 13.34e+00 13.34e+00 13.34e+00 13.34e+00 13.34e+00 13.34e+00 13.34e+00 13.34e+00 13.34e+00 13.34e+00 13.34e+00 13.34e+00 13.34e+00 13.36e+00 13.36e+00 13.36e+00 13.36e+00 13.36e+00 13.36e+00 13.36e+00 14.37e+00 15.36e+00 16.36e+00 17.36e+00 17.36e+00 18.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00 19.36e+00	1.25e+C 1.25e+C 1.25e+C 1.25e+C 1.62e+C 1.62e+C 1.62e+C 1.62e+C 1.62e+C 1.62e+C 1.62e+C 1.62e+C 1.62e+C
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TRANSCRIPTION FACTOR H 4.44 HYPOTHETICAL 31.9 KD P 4.44 VIRAL PROTEIN TPX.  VIRAL PROTEIN TPX.  VIRAL PROTEIN TPX.  CTOCHROME B (EC 1.10.  REGILATORY PROTEIN E2.  ALMA CARBAMOYL-PHOSPHATE SY 4.44 CARBAMOYL-PHOSPHATE SY 4.44  MINOR CAPSID PROTEIN L 4.44  CANDOMERASE II-ASSOC 4.44  CAMP-DEPRUBENT 3', 5'-C 4.44  TOPOISOMERASE II-ASSOC 4.44  CYTOKINE RECEPPOR COMM 4.44  ATROPHIN-1 (DENTATORUE 4.44	82	CUTHERIA: PRIMATES.  RU SEQUENCE FROM N.A.  RC TISSUE-PLACENTA;  RX MEDILINE; 96181295.  RA CONDER TES. 56:1498-1502(1996).  RL CANER RES. 56:1498-1502(1996).  RD SCHAFER H., TRAUZOLD A., LETTAU P., KALTHOFF H., FOELSCH U.R.,  RA SCHAFER H., TRAUZOLD A., LETTAU P., KALTHOFF H., FOELSCH U.R.,  RA SCHADIT W.E.;  RA SCHADIT W.E.;  RA GASTROBATEROLOGY 0:0-0(1997).  RN [3]  RP PIETZSCH A., BUECHLER C., ASLANIDIS C., SCHMITZ G.;  RA PIETZSCH A., BUECHLER C., ASLANIDIS C., SCHMITZ G.;  RA PIETZSCH A., BUECHLER C., ASLANIDIS C., SCHMITZ G.;  RA PIETZSCH A., BUECHLER C., ASLANIDIS C., SCHMITZ G.;  RA PIETZSCH A., BUECHLER C., ASLANIDIS C., SCHMITZ G.;  RA HILLIER L., CLARK N., DUBUGUE T., ELLISTON K., HAWKINS M., HOLMAN M.,  RA HILLIER L., CLARK N., DUBUGUE T., ELLISTON K., HAWKINS M., HOLMAN M.,  RA HILLIAMSON A., WORLDMANN P., WILCOON R.,  RA WILLIAMSON A., WORLDMANN P., WILCOON R.,  SUBMITTED (FEB-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.  CC -:- INDUCTION: BY RADIATION, TPA, OKADAIC ACID AND TNF-ALPHA.
	2.100e+01 2.100e+01 2.100e+01 2.100e+01 3.100e+01 3.100e+01 3.100e+01 3.100e+01 3.100e+01 3.100e+01 3.100e+01 3.100e+01 3.100e+01 3.100e+01 3.100e+01 3.100e+01 3.100e+01 3.100e+01 3.100e+01 3.100e+01	2. 2. 4. 4. 4. 4. 4. 4. 4. 4. 4. 4. 4. 4. 4.
NITRATE REDUCTASE (EC PROTEIN-TYROSINE PHOSP PROTEIN FOR BAGTERED PRECURSOR PHOSPHOLIPASE C ACCES CAT PROTEIN (CAPSID PROTEIN CAPSID PROTHENTER 34.2 KD PROTHENT ROTHEN UL49 PYPOTHENE B (EC 1.10. CYTOCHROME B (EC 1.10. BLORGE-GATED PROTEIN L VOLTAGE-GATED PROTEIN L NOLTAGE-GATED POTASSIU RAS-RESPONSIVE ELEMENT INTERLEUKIN-3 RECEPTOR BRIDE OF SEVENLESS PROLIN-36 PROTEIN.  CSA PERTIDASE PRECURSO FORMIN (LIMB DEFORMITY BETA-MANNANAE / ENDOG		BETA-HENCSAMUNDASE BE BETA-HENCSAMUNDASE BE BETA-HENCSAMUNDASE BE BENCSTORN G/4 SVNT GO KD WAS ANTIGEN BY A STATEMENT BY BY A STATEMENT BY A STATEMENT BY A STATEMENT BY A STATEMENT BY A
NIAL HORVU PTPJ_MOUSE VP06_BPPRD BGT7_SHEEP PSAD_HORVU PLCR_BSEAC COAT_MCNV IL49_HSVBP YL58_CAEL CYBB_STEAT LI3B_MOUSE BOSS_DROVI LI3B_MOUSE BOSS_DROVI LI3B_MOUSE BOSS_DROVI LI3B_MOUSE BOSS_DROVI LI3B_MOUSE BOSS_DROVI LI3B_MOUSE BOSS_DROVI CKPA_STRPY FORM_CHICK	YFA7_YEAST POLK_TYWV POLK_TYWV HMCU_DROME H5_ANSAN VYP10_BPPRD YO91_NPVAC COAT_CSWV COAT_CSWV FRTI_HUWAN V290_ASFL5 FRAZ_WOUSE VCOM_ADE12 MYCL_HUWAN YJGP_EOLI VGLM_EBV TEF3_HUWAN G3PT_MOUSE B1AT_MOUSE B1AT_MOUSE R123_HUWAN G3PT_MOUSE R2F1_HUWAN G3PT_MOUSE R124_RACM G3PT_MOUSE R124_RACM G3PT_MOUSE R124_RACM G3PT_MOUSE R124_RACM G3PT_MOUSE R124_RACM G3PT_MOUSE R124_RACM G3PT_MOUSE R124_RACM G3PT_MOUSE R124_RACM G3PT_MOUSE R124_RACM G3PT_MOUSE R124_RACM G3PT_MOUSE R124_RACM G3PT_MOUSE R124_RACM G3PT_MOUSE R124_RACM G3PT_MOUSE R124_RACM G3PT_MOUSE R124_RACM G3PT_MOUSE R124_RACM G3PT_MOUSE R124_RACM G3PT_MOUSE R124_RACM G3PT_MOUSE R124_RACM G3PT_MOUSE R124_RACM G3PT_MOUSE R124_RACM G3PT_MOUSE R124_RACM G3PT_MOUSE R124_RACM G3PT_MOUSE R124_RACM G3PT_MOUSE R124_RACM G3PT_MOUSE R124_RACM G3PT_MOUSE R124_RACM G3PT_MOUSE R124_RACM G3PT_MOUSE R124_RACM G3PT_MOUSE R124_RACM G3PT_MOUSE R124_RACM G3PT_MOUSE R124_RACM G3PT_MOUSE R124_RACM G3PT_MOUSE R124_RACM G3PT_MOUSE R124_RACM G3PT_MOUSE R124_RACM G3PT_MOUSE R124_RACM G3PT_MOUSE R124_RACM G3PT_MOUSE R124_RACM G3PT_MOUSE R124_RACM G3PT_MOUSE R124_RACM G3PT_MOUSE R124_RACM G3PT_MOUSE R124_RACM G3PT_MOUSE R124_RACM G3PT_MOUSE R124_RACM G3PT_MOUSE R124_RACM G3PT_MOUSE R124_RACM G3PT_MOUSE R124_RACM G3PT_MOUSE R124_RACM G3PT_MOUSE R124_RACM G3PT_MOUSE R124_RACM G3PT_MOUSE R124_RACM G3PT_MOUSE R124_RACM G3PT_MOUSE R124_RACM G3PT_MOUSE R124_RACM G3PT_MOUSE R124_RACM G3PT_MOUSE R124_RACM G3PT_MOUSE R124_RACM G3PT_MOUSE R124_RACM G3PT_MOUSE R124_RACM G3PT_MOUSE R124_RACM G3PT_MOUSE R124_RACM G3PT_MOUSE R124_RACM R124_RACM R124_RACM R124_RACM R124_RACM R124_RACM R124_RACM R124_RACM R124_RACM R124_RACM R124_RACM R124_RACM R124_RACM R124_RACM R124_RACM R124_RACM R124_RACM R124_RACM R124_RACM R124_RACM R124_RACM R124_RACM R124_RACM R124_RACM R124_RACM R124_RACM R124_RACM R124_RACM R124_RACM R124_RACM R124_RACM R124_RACM R124_RACM R124_RACM R124_RACM R124_RACM R124_RACM R124_RACM R124_RACM R124_RACM R124_RACM R124_RACM R124_RACM R124_RACM R124_RACM R124_RACM R124_RACM R124_RACM R124_RAC	HEXB_HUMAN PERTL_ECOLI V70K_TYMVA GIDA_HAEIN GIDA_HAEIN GIDA_ECOLI DMK_HUMAN T2DS_HAT T2DS_RAT T2DS_RAT T2DS_MOUSE PSF_HUMAN BS11_TRYCR BS11_TRYCR BS11_TRYCR BS11_TRYCR DYN3_RAT YROL_YEAST T2D3_HUMAN BS11_TRYCR DYN3_RAT YROL_YEAST T2D3_HUMAN SS10_NOUSE SSC_MOUSE SSC
		5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 5056 1 50
		<i>หายเกลา เกลา เกลา เกลา เกลา เกลา เกลา เกลา </i>
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Gaps

DOMAIN CARBOHYD CONFLICT CONFLICT SEQUENCE

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" Match

61 61 121

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61 RSRRVLYPRVVRRQLPTEEPNIAKRVLFLLFAIIFCQILMAEEGVSQPLAPEDATSAVTP 120
                                                                  1 MCHSRNHLHTMTGLRAPSPAPSTGPELRRGSGPEIFTFDPLPERAVVSTARLNTSRGHRK 60
                                                                                        VIRIDAE; DS-DNA NONENVELOPED VIRUSES; ADENOVIRIDAE; MASTADENOVIRUSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 THR-PRO REPEATS REGIONS AND TWO NEAR IDENTICAL REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPINDLER K.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                349 IPTPIPIPIPIPIPIPIPIPIVINITYVVF-DVIPSPIPIPIPIPIPIPIPIPIPIPIPIPIP 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 PIMILLOAPIPAPSTIPGPRRGSGPEIFTFDPLPEPAAAPAGRPSASRGHRRSRRVLYP
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7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 117; DB 1; Length 474
Pred. No. 2.12e-03;
26; Mismatches 62; Indels
                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEISSNER J.D., HIRSCH G.N., LARUE E.A., FULCHER R.A.,
SUBMITTED (MAY-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL, 20101333; -.
CORE PROFEIN; LATE PROTEIN.
SEQUENCE 228 AA; 25571 MW; DE97BB3A CRC32;
                                                                                                                                                                                                                                                                                                                VTP 3
VTP37171V
STANDARD; PRT; 474 AA.
P19275;
01-NOV-1990 (REL. 16, CREATED)
01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
01-REB-1991 (REL. 17, LAST ANNOTATION UPDATE)
VIRAL PROTEIN TPX.
THERMOPROTEUS TENAX VIRUS 1 (STRAIN VT3) (TTV1).
                              22; Mismatches 19;
              Pred. No. 3.93e-121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    467 THR-PRO(N).
49507 MW; BAC5D831 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              010442;
01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
MINOR CORE PROTEIN (PROTEIN V).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                228 AA
                                                                                                                                                                                                                    121 EPISAPITAPPVLEPLNITSESSDYALDLKAFL 153
| :|:: |||||:|||||:||
121 AP--TPVS--PVLEPFNITSEPSDYALDLSTFL 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE, 9024566.
MEDLINE, 9024566.
MUCHLIG W.;
NUCLEIC ACIDS RES. 18:2171-2171(1990).
EMBL; X14717; E1192689; -.
EMBL; X16717; E1192686.
PIR; S06686; S06686.
PIR; S15921; S15921.
REPEAT. 278 467 3 THR-PRO R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            THR-PRO(N).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  THR-PRO(N)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOUSE ADENOVIRUS TYPE 1 (MAV-1)
          Local Similarity 70.6%; tes 108; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match
Best Local Similarity 23.7%;
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        278
368
378
437
447
474 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 4

ID VCOM_ADEM1

AC 010442;

DT 01-NOV-1997

DT 01-NOV-1997

DT 01-NOV-1997

DT 01-NOV-1997

DT 01-NOV-1997

DT 01-NOV-1997

OC VIRIDAE; DS-

RN (1)

RN (1)

RN SEQUENCE FO

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SUBMITTED (M

CORE POSTEN

SO SEQUENCE Z
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REPEAT
SEQUENCE
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            Best Loc
Matches
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CELL CYCLE.

CHORDING TYPE II MEMBRANE PROTEIN (POTENTIAL).

CHORDING SECRETICITY: EXPRESSED PREDOMINANTLY IN THE LUNG, TESTES AND THE UTERUS.

CHORDING S.

CHORDING S.

CHORDING STRONG.

CHORDING STRONG.
                                                                                                                                                                                                                                                                                                                                                                                              ö
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MEDLINE; 93173526.
CHARLES C.H., YOON J.K., SIMSKE J.S., LAU L.F.;
ONCOGENE 8:797-801(1993).
-I- FUNCTION: NOT KNOWN; EXPRESSED DURING THE GO-G1 TRANSITION OF THE
                                                                                                                                                        SIGNAL-ANCHOR.
CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RSRRVLYPRVVRRQLPVEEPNPAKRLLFLLLTIVFCQILMAEEGVPAPLPPEDAPNAASL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MCHSRSCHPTMTILQAPTPAPSTIPGPRRGSGPEIFTFDPLPEPAAAPAGRPSASRGHRK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IEXI_MOUSE STANDARD; PRT; 153 AA.
P46694.
01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 34, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
PROJIEIN "INDUCIBLE IMMEDIATE FARLY GENE IEX-1 (IMMEDIATE EARLY PROTEIN GLY96) (IMMEDIATE EARLY RESPONSE 3 PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MUS MUSCULUS (MOUSE).
TUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
-!- PTM: GLYCOSYLATED.
-!- SIMILARITY: STRONG, TO MOUSE ORTHOLOG.
-!- CAUTION: REF.4 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO FRAMESHIFTS.
                                                                                                                                                                                                                                                                                                                                                    Score 1114; DB 1; Length 156; Pred. No. 3.79e-194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 153;
                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                            (POTENTIAL).
EXTRACELLUIAR (POTENTIAL).
ADOUBNIAL.
A - G (IN REF. 1).
P -> R (IN REF. 1).
W, 46013510 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EXTRACELLULAR (POTENTIAL)
POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APTPVSPVLEPFNLTSEPSDYALDLSTFLQQHPAAF 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7A284EC2 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67.5%; Score 752;
                                                                            EMBL; S81914; G1488385; --
EMBL; Y96438; E356480; --
EMBL; Y14551; E333102; --
EMBL; T49531; -; NOT_ANNOTATED_CDS.
GLYCOPROTEIN: TRANSMEMBRANE; SIGNL-A
DOMAIN
TRANSMEM
83
99
SIGNAL-A
SIGNAL-A
                                                                                                                                                                                                                                156 EX
133 PO
54 A
106 P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16875 MW;
                                                                                                                                                                                                                                                                                                                                                  Match 100.0%;
Local Similarity 100.0%;
les 156; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        153
                                                                                                                                                                                                                                100
133
54
106
156 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (1)
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            153 AA;
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RESULT ID DE DE DE DE PRA DE P

DOMAIN CAPBOHYD

SEQUENCE Query Match

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LIMB BUD
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                                                                                                                                                                                                                                                                                                                        WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FRASER A.,
FOLTON L., GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M.,
JOHNSTON L., JONES M., KERSHAW J., KIRSTER J., LAISSTER N.,
LATREILLE P., LIGHTNING J., LLOYD C., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PEROY C., RIFKEN L., ROOPER A., SAUNDERS D., SHOWKEEN R.,
SIMS M., SMALDON N., SMITH A., SMITH M., SONNHAMMER E., SIADEN R.,
WATERSON R., WATSON A., WEINSTOCK L., WILKINSON-SPROAT J.,
                                                     123 PPAVP-PPRAVPPVGVRYHPSIEVARPPAARISPPR-RRRRRRSPRPRATAAYRSSAEV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 844 FLENRGRIPSTSSAPSTSENPPGPSFNS-EDAADIRAGRLPLGTRPNRRTVRETVHPAAA 902
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             903 araespnhisliftätthtfapagf-plamassnvpstsagppgwpirqvvsptpttrgl 961
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                                 Gaps
                                                                                                                                                                                                                                                                  EUKARYOTA; METAZOA; ACOELOMATES; NEMATODA; SECERNENTEA; RHABDITIDA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 109; DB 1; Length 1799; Pred. No. 2.51e-02;
         Length 228;
       Score 112; DB 1; Length 228
Pred. No. 1.01e-02;
21; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30; Mismatches 65; Indels
                                                                                                                                                                                          01-FEB-1994 (REL. 28, CREATED)
01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
15-UUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
4.PPOTHETICAL 202.6 KD PROTEIN ZK688.5 IN CHROMOSOME III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36 UBIQUITIN-LIKE.
202641 MW; 3EF7DDB2 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FOR4_MOUSE STANDARD; PRT; 1206 AA. 005859, 01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE) 01-JUN-1994 (REL. 39, LAST SEQUENCE UPDATE) 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE) LD.
                                                                                                                                                                      1799 AA
                                                                                                 181 VERRRRVAQTVPVVRYHPSIQVEPAVHPPLAP 212
                                                                                                                       81 NPAKRLLFLLLIV-FCOILMAEEGVPAPLPP 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                      NATURE 368:32-38(1994).
EMBL; L16621: G289783; -.
PRIP: S44920.
WORMPEP: 2K688.5; CE00463.
PROSITE; PS50053; UBIQUITIN_2; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 9.8%; bocal Similarity 23.7%; es 31; Conservative
       Cuery Match 10.1%;
Best Local Similarity 29.3%;
Matches 27; Conservative
                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                     AENORHABDITIS ELEGANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYPOTHETICAL PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1799 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            962 FEFDLSGSSDQ 972
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130 EPFNLTSEPSD 140
                                                                                                                                                                                                                                                                                                    STRAIN-BRISTOL N2;
MEDLINE; 94150718.
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YO25_CAEEL
P34675;
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-1. FUNCTION: IS IMPORTANT IN THE MORPHOGENESIS OF LIMB AND MAY HAVE A FUNCTION IN DIFFERENTIATED CELLS OR BE INVOLVED IN MAINTAINING SPECIFIC DIFFERENTIATED STATES.
-1. TISSUE SPECIFICITY: IT IS FOUND THROUGHOUT THE EMBRYO BUT HAS A FUNCTIONAL ROLE ONLY IN THE KIDNEY AND LIMB.
-1. DEVELOPMENTAL STAGE: THIS IS THE ISOSOME FOUND IN THE DEVELOPING ECTODERMAL RIDGE AND THE MESENCHYMAL COMPARTMENT OF THE DEVELOPING
                                                                                                                                                                                                                                                                                                                                                                                                     ALTERNATIVE PRODUCTS: MANY DIFFERENT FORMS OF THIS PROTEIN ARE PRODUCED BY ALTERNATIVE SPLICING OF THE LD GENE. A VARIATION IN SPLICING IS SEEN AMONG DIFFERENT TISSUES AND DIFFERENT SIZE TRANSCRIPTS EXIST WITHIN ANY ONE TISSUE. THIS IS ISOFORM 4 AND IS DIFFERENT IN ITS N-TERMINAL TO THE OTHER MOUSE ISOFORMS SO FAR DETERMINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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005860;
01-JUN-1994 (REL. 29, CREATED)
01-JUL-1998 (REL. 29, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
FORMIN (LIMB DEFORMITY PROTEIN)...
FON SILD.
MUS MUSCULUS (MOUSE).
EUTHERIA; RETAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MANMALIA;
MUS MUSCULUS (MOUSE).
EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA;
EUTHERIA: RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEAR PROTEIN; DEVELOPMENTAL PROTEIN; ALTERNATIVE SPLICING.
DOMAIN 635 638 POLY-SER.
DOMAIN 644 744 PRO-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 103; DB 1; Length 1206;
Pred. No. 1.50e-01;
15; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 716 VLALPNSGGPPP-PPPPPPPPGLAPPP-PPGL-SFGLSSSSGYP 758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             751 755 POLY-SER.
1206 AA; 133464 MW; 6D70C261 CRC32;
                                                                                                                                                                       KUO A., LEDER P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 9.2%;
Local Similarity 39.1%;
les 18; Conservative
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TISSUE-KIDNEY, AND TESTIS:
MEDLINE; 90363291.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X62379; G51553; -
PIR; S24407; S24407.
HSSP; P19999; 1CLG.
                                                                                                                                                                                           GENES DEV. 6:29-37(1992)
                                                                                                                                         MEDLINE; 92112033.
GRUSBY-JACKSON L.,
                                                                                                 SEQUENCE FROM N.A.
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Drosophila melanogaste Drosophila melanogaste Humo sapiens chromosom Human Chromosome 4 (cl. human STS SHGC-51059, Sequence 5 from patent Human Ul small nuclear Mus musculus glycosylp Gallus gallus glbrobla S.scrofa mRNA for L-36 BOVine inorganic pyrop	Dirotharia immitts 70 Mus musculus mRNA for Xenopus laevis nuclear Dictyostelium discoide H.sapiens mig-5 gene. Rana catesbelana allan	Danio rerio stem cell S.scrofa mRNA for inte Zea mays LONI protease Cyl-1-cyclin DI [mice, Xenopus laevis myb-rel	Homo sapiens Cdc14Bl p Rattus norvegicus AMPA *** SEQUENCING IN PROG human STS SHGC-15668. SHGC-57073 Human Homo Drosophila melanogaste	Homo sapiens full leng laminin receptor homol Homo sapiens clone 246	Casein Kinase 2 alpha Drosophila melanogaste Human clone 23960 mkNA	M.musculus sebt mrNA. Mouse mrNA for prothro CDNA encoding alpha 2,	Rattus norvegious UDP- Dictyostellum discoide Sequence I from patent Homo sapiens tyrosine Homo sapiens transcrip	Dictyostelium discoide Human trans-Golgi p230 Caenorhabditis elegans S.pombe chromosome II Arabidopsis thaliana g	Homo sapiens DNA seque Caenorhabditis elegans homos eme utaliale	human STS WI-13613.  human STS WI-13630.  Mus musculus nuclear o  Mus musculus long inte	B. Verrucosa Bet v 1g m B. Verrucosa Bet v 1b m A. thallana mRNA for Cu Danio rerio mRNA for d Mus musculus probasin	Rattus norvegicus pren P.reticulata Mhc gene,	Pleuronectes americanu Oryza sativa glutathio X.laevis mRNA for Xven	cGATA-3 [chickens, liv C.elegans mRNA for p34	Pisum sativum mRNA for LW H.echinata mRNA for LW H.echinata mRNA for LW H.echinata mRNA for LW	Human eukaryotic initi Homo sapiens (clone S2 Homo sapiens clone 247 Lucilia cuprina alpha
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10772 18 74371 218 192 30 202 30 203 30 205 21 205 21 3436 28 1125 19 1125 19	1294 18 1479 28 1811 20 1840 18 1941 25 2116 20	2873 20 3042 19 3217 24 3737 28 3789 20	4624 26 5433 28 224645 17 232 30 350 30 571 18	648 26 739 25 1332 26	1435 18 1639 26	1908 28 2031 28 2179 21	2301 2624 2628 3946	5061 7695 38890 42934 58527	118226	500 500 500	714 718 802 803	861 884	907 945 977	1216	1362	1452 1588 1727 2240
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	se 3.1A John F. Collins, Biocomputing Research Unit. ight (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd	n n.a n.a. database search, using Smith-Waterman algorithm Sun Jan 10 02:36:53 1999; MasPar time 2001.26 Seconds 0utput not generated.	Title:       >US-08-799-910-9         Description:       (1-1228) from USO8799910.seq         Perfect Score:       1228         N.A. Sequence:       1 ATGTGTCACTCTCGCAGCTGAAAAAAAAAAAAA	TABLE default Gap 6	: Dbase 0; Query 0	inimum Match 0% isting first 200 summaries	embl55 1:em_ba 2:em_fun 3:em_htg 4:em_huml 5:em_hum2 6:em_in 7:em_om 8:em_or 9:em_ov 10:em_pat 11:em_ph 12:em_pl 13:em_ro 14:em_vi	genbank107 15:92_ba1 16:92_ba2 17:92_htg 18:95_tn 19:92_om 20:92_ov 21:92_pat 22:95_ph 23:92_pl1 24:95_pl2 25:92_pr1 26:92_pr2 27:92_pr3 28:92_ro 29:92_st 30:92_sts 31:92_sy 32:92_un 33:92_v1	Mean 11.515; Variance 7.482; scale 1.539	. No. is the number of results predicted by chance to have a e greater than or equal to the score of the result being printed, is derived by analysis of the total score distribution.	SUMMARIES Query Match Length DB ID Description Pred. No.	98.1 1230 26 HSDIF2 Homo sapiens mRNA for 0	95.4 1223 25 581914 IEX-1=radiation-induci 79.5 1309 27 AF039067 Homo sapiens anti-deat 74.7 1864 26 HSPRGI H.sapiens PRGI gene.	38.4 477.27 AF083421 Homo saplens radiation 7 25.5 343.26 HSA227914 Homo saplens partial m 3 25.5 343.29.29 Homosaplens partial m 3	9.3 1758 28 RNPRG1 R.HOCVEGICUS 9.75 20 HANN. 9.5 1758 28 RNPRG1 R.HOCVEGICUS PRG1 GM. 9.7 1758 21 166494 Sequence 14 from paten 9 5 7 718 21 166494 Sequence 14 from paten 9 5 7 718 21 166494	14 Irom paten b 5 from patent 4 1ens dlf-2 gen 4 iens chromosom 1

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RNA. RESA. - cat - cat 130m 130m thro pxen pxen pxen pxen	fro fro fro fro fro fro fro fro fro fro	PROG PROG PROG PROG PROG PROG ***	5	.a; Eut G. Gocyte/ to	lipopolysaccharide, ceramide, and lysophosphatidylcholine Biochem. Blophys. Res. Commun. 235 (1), 4-9 (1997) 27339426 (1997) Parachem. Blophys. Res. Commun. 235 (1), 4-9 (1997) 2 (bases 1 to 1230) Pietzsch.A.  Direct Submission Submission Blooratory Medicine, University of Regensburg Chemistry and Laboratory Medicine, University of Regensburg Chemistry and Laboratory Medicine, University of Regensburg Starars-Osef-Strauss-Allee 11, 93053 Regensburg, FRG Nondratyev, A.D., Chung, K.N. and Jung, M.O. Indentification and characterization of a radiation-inducible Glacostylated human early-response gene Cancer Res. 56 (7), 1498-1502 (1996)
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X.xiphidium Xsrc mRNA. P.falciparum FC27 RESA Gallus gallus beta-cat Human UZAFBFL gene. Co HOMO saplens Cyclin-D Mus musculus peroxisom Human mRNA for erythro Expression vector pXen Expression vector pXen Expression vector pXen Expression vector pXen Homo saplens ealf-1 rel Mus musculus maten	Feline syncytal virus Caenorhabditis elegans Caenorhabditis elegans S.pombe chromosome I c Schizosaccharomyces po Human DNA sequence fro Human DNA sequence fro Arabidopsis thaliana c Caenorhabditis elegans *** SEQUENCING IN PROG Human Chromosome X, co	### SEQUENCING IN PROG Homo sapiens XP22 bins *** SEQUENCING IN PROG Homo sapiens chromosom *** SEQUENCING IN PROG Human BAC clone RG020D *** SEQUENCING IN PROG *** SEQUENCING IN PROG Homo sapiens Chromosom Homo sapiens Chromosom Homo sapiens Chromosom Homo sapiens Chromosom	Mus au Mus au Homo s	protein. a; Vertebr dae; Homo. ization of ization of	235 (1) 225 (1) 225h, 1 ne, Uni 3053 Re Jung, h tiong, h
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                                                                                                                                                                                                 GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 177109] from the original journal article. This sequence comes from Fig. 2A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CICCCGGAGCCCGCAGCGGCCCCTGCCGGGCGCCCCCAGCGGCTCTCGCGGGCACCGGAAG 198
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                                                                                                                                                                                                                                                                                                                                                 gene; This
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        12-AUG-1996
                                                                                                   Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 1233)

Rondratyev,A.D., Chung,K.N. and Jung,M.O.
Identification and characterization of a radiation-inducible glycosylated human early-response gene
Cancer Res. 56 (7), 1498-1502 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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/note="radiation-inducible immediate-early
sequence comes from Fig. 2A"
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IEX-1-radiation-inducible immediate-early mRNA Partial, 1223 nt].
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Pred. No. 0.00e+00;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                            /note="radiation-inducible
/gene="IEX-1"
19. .489
                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
19. .489
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Best Local Similarity 99.4%;
Matches 1198; Conservative
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Homo saplens anti-death protein (IEX-1L) mRNA, complete cds.
AF039067
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             CGAGAGGGTATCCCCAACTGGGACTTCCGAGGCAACTTGAACTCAGAACACTACAGGGGA
                                                                                   GACGCCACCCGGTGCTTGAGGCGGGACCGAGGCGCACAGAGACCGAGGCGCATAGAGACC
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CCCGCACTCCCCAAAAAAATCCGAAAAACCACAAAAAACACCAGGCGTACCTGGTGCG
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Primates, Catarihini, Hominidae, Homo.
1 (bases 1 to 1309)
Wu,M.X., Ao.Z., Prasad.K.V.S., Wu,R.
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23-SEP-1997

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AAAPAGRPSASRGHRKRSRRVLYPRVVRRQLPVEEPNPAKRLLFLLTIVFCQILMAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   revised by [4]
C (bases 1 to 508)
Schaefer, H., Trauzold, A., Lettau, P., Kalthoff, H., Foelsch, U.R. and
Schmidt, W.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDNA cloting and sequencing of a novel human early response gene and characterization of its expression in pancreatic carcinoma
                                                                                                            1040 CGGGTGGGGGAGGACGTCCCGGCTGGGATGAAGTCTGGTGGTGGGTCGTAAGTTTAGGAG 1099
                                                         1100 GIGACIGCAICCICCAGCAICICCAACICCGICIGICIACIGIGIGAGACIICGGCGGACC 1159
                                                                       Homo sapiens
Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 1864)
Trauzold,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (23-SEP-1997) H. Schaefer, Trauzold, Laboratory of
Molecular dastroenterology, 1st Dept.of Medicine, University
Kiel, Schittenhelmstrasse 12, Kiel, D-24105, FRG
On Sep 27, 1997 this sequence version replaced gi:1515291.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (OS-MAR-1996) A. Trauzold, Laboratory of Molecular
Gastroenterology, 1st Dept.of Medicine, University of Kiel,
Schittenhelmstrasse 12, Kiel, D-24105, FRG
                                                                                                                                                                                1111 GAGGTAGAGGGTTGGGGGTTGGGGGTGTCACGGAGCGACTGTCGAGATCGCCTAGTAT
                  1220 GAGGTAGAGGGTTGGGGGGTTGGTGGCGTCACGGAGCGACTGTCGAGATCGCCTAGTAT
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/db_xref="taxon:9606"
/cell_line="818-4"
1. .562
                                                                                                                                                                                                                       /gene="PRG1"
/563. And
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Schaefer, H.
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/gene="PRG1"
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PRG1 gene.
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AAAPAGRPSASRGHRRRSRRVSLPSSGEYRRSGHSRCALPWSHWGTTRLOSLDITCLL
FCLPLVRRQLPVEEPRNAKRLELLLITIVFCGILWAEEGVPAPLPPEDAPNASLAPT
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Submitted (17-DEC-1997) Tumor Immunology, Dana Farber Cancer Institute, 44 Binney Street, Boston, MA 02115, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                    271 CICACCATCGTCTTCTGCCAGATCCTGATGGCTGAAGAGGTGTGCCGGCGCCCCTGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                          Score 976; DB 27; Length 1309;
Pred. No. 0.00e+00;
0; Mismatches 0; Indels 2
                                                                                                          7. 582
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1. .1309
                                                                                    1. .1309
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/gene="PRG1"
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Pred. No. 0.00e+00;
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/gene="PRG1"
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/translation="MCHSRSCHPTMTILQAPTPAPSTIPGPRRGSGPEIFTFDPLPEP
AAAPAGRPSASRGHRKRSRRVLYPRVVRRQLPVEEPUPAKRLLFLLTIVFCQILMAE
EGVPAPLPPEDAPNAASLAPTPVSPVLEPFNLTSEPSDYALDLSTFLQQHPAAF"
                                                                                                                   IEX1
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                                                                                                                                                                                                                                       Eutheria;
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Identification and characterization of a radiation-inducible glycosylated human early-response gene
Cancer Res. 56 (7), 1498-1502 (1996)
                                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 477)
Kumar,R., Kobayashi,T., Warner,G.M., Wu,Y., Salisbury,J.L.,
Lingle,W. and Pittelkow,M.R.
A Novel Immediate Early Response Gene, IEX-1 Is Induced by
Ultraviolet Radiation in Human Keratinocytes
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/cell_type="keratinocyte; fetal osteoblast"
1. 477
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Eukaryota; Metazoa; Chordata; Vertebrata;
Primates; Catarrhin; Hominidae; Homo.
1 (bases 1 to 477)
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Direct Submission
Submitted (11-AUG-1998) Nephrology Reseas
Street SW, Rochester, MN 55905, USA
Location/Qualifiers
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/citation=[1]
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CTCCCGGAGCCCGCAGCGGCCCCTGCCGGGCGCCCCAGCGCCTCTCGCGGGCACCGAAAG 186
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1 (bases 1 to 343)
Dominguez,O., Ashhab,Y., Sabater,L., Belloso,E., Caro,P. and Pujol-Borrell,R.
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                                             CGCAGCCGCAGGGTTCTCTACCCTCGAGTGGTCCGGCGCCCAGCTGCCAGTCGAGGAACCG
                                                        GCTGAAGAGGGTGTGCCGGCGCCCCTGCCTCCAGAGGACGCCCCTAACGCCGCATCCCTG
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Pred. No. 3.31e-173;
0; Mismatches 7; Indels 3;
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Homo sajlens partial mRNA; ID YG40-2.
93183967
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/db_xref="taxon:9606"
/dev_stage="adult"
/cell_type="T lymphocyte"
/cell_line="T122.12"
/clone="PH19-20, PH19-21"
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Best Local Similarity 97.1%;
Matches 333; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 (bases 1 to 343)
Dominguez, C.
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                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
                                                                                                                                                                                                                                                                                                                                                              human.
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ACCESSION
NID
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SOURCE
ORGANISM
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REFERENCE
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TITLE
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                     121
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AUTHORS
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127
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Submitted (29-JUL-1992) L. Lau, University of Illinois College of Med., Dept. of Genetics, M/C 669, 808 South Wood Street, Chicago, IL 60612, USA.

2 (bases I to 1938)
Charles, C.H., Yoon, J.K., Simske, J.S. and Lau, L.F.
Genomic structure, CDNA sequence, and expression of gly96, a growth factor-inducible immediate-early gene encoding a short-lived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
                                                                                                                                              CCCTCCACCATCCCGGGACCCCGGCGGGGCTCCGGTCTGAGATCTTCACCTTCGACCCT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CGGCGGACCATTAGGAATGAGATCCGTGAGATCCTTCCATCTTCTTGAAGTCGCCTTTAN 237
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922 GGGAGGACTCGGGTGGGGGAGGACGTCCCGGCTGGGATGAAGTCTGGTGGTGGTGGTCGTAA 981
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Pred. No. 6.27e-50;
0; Mismatches 47;
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/organism-*Mus musculus"
/strain-*BALB/c"
/db_xref-*taxon:10090"
a 525 c 503 g 520
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93173526
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M.musculus gly96 mRNA.
X67644
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Best Local Similarity 77.8%;
Matches 165; Conservative
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1 (bases 1 to 1938)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lau, L.
Direct Submission
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RESULT

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1166 TAGGGGATCTCGACAGTCGCTCCGTGACACCCCACCCCCAACCCTTGCTCGCAG 1107
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                                                                                                                                                                                                             219 CCAGCIGCCAGTGCAACCAAAAGGTICITTTTTGTGCTCACCAT
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                        DB 21; Length 7218;
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                       6.4%; Score 79; DB 21; Length 721
Similarity 1.3%; Pred. No. 9.39e-27;
5; Conservative 220; Mismatches 146; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (Dases 1 to 7218)
Dorner,F., Scheiflinger,F. and Falkner,F.Gunter.
Recombinant fowlpox virus
Patent: US 5670367-A 14 23-SEP-1997;
Location/Qualifiers
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1491 c 1486 g
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Matches 9; Conserv
                                      Local Similarity
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FEATURES
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                                                                                                                                       1 (bases 1 to 1758)
Schafer, H., Trauzold, A., Siegel, E.G., Folsch, U.R. and Schmidt, W.E.
PRG1: a novel early-response gene transcriptionally induced by
pituitary adenylate cyclase activating polypeptide in a pancreatic
carcinoma cell line
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                                                                                               Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 CCCTCCACCATCCCGGGACCCCGGGGGCTCCGGTCTTCACCTTCGACCT 120
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 03-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                               Submitted (05-MAR-1996) A. Trauzold, Laboratory of Molecular Gastroenterology, 1st Dept.of Medicine, University of Kiel, Schittenhelmstrasse 12, Kiel, D-24105, FRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ATGIGICACTCTCGCAGCTGCCACCGACCATGACCATCCTGCAGGCCCCGGACCCGGGCC
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Dorner,F., Schelflinger,F. and Falkner,F.Gunter.
Recombinant fowlpox virus
Patent: US 5670367-A 14 23-SEP-1997;
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 800
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Pred. No. 1.67e-47;
                                                                                                                                                                                                                                                                                                                 Location/Qualifiers

1. 1758
/organism="Rattus norvegicus"
/db_xref="taxon:10116"
/cell_line="AR4-2J"
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1491 c 1486 g
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  ΝA
 bp
gene.
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590. .1279
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475 c
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Best Local Similarity 76.9%;
Matches 163; Conservative
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                                         91515318
PRG1 gene.
Norway rat.
Rattus norvegicus
 RNPRG1 1758
R.norvegicus PRG1
X96437
                                                                                                                                                                                                                                                                     Direct Submission
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ACCESSION
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FEATURES
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ORIGIN
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AUTHORS
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AUTHORS
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AC005369 74371 bp DNA PRI 01-AUG-1998
Homo sapiens chromosome 5, BAC clone 119j3 (LBNL H175), complete
sequence.
AC005369
93367505
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Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Frimates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 74371)
Kimmerly,W., Bondoc,M., Cheng,J., Connolly,K.S., Gunning,K.M., Kadner,K., Miguel,T., Miller,C., Pitluck,S., Pollard,M., Sojeski,H., Subramanian,S. and Martin,C.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Large Scale Sequence Analysis and Annotation with the Sequence Comparison Analysis (SCAN) System
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (01-AUG-1998) Human Genome Center, DOE Joint Genome Institute, Lawrence Berkeley National Laboratory, MS 74-157, Berkeley, CA 94720, U.S.A.
Sequence submitted by:
DOE Joint Genome Institute.
Direct Submission
Submitted (27-FEB-1998) A. Pietzsch, Institute for Clinical
Submitted (27-FEB-1998) A. Pietzsch, University of Regensburg,
Franz-Josef-Strauss-Allee 11, 93053 Regensburg, FRG
Related sequences: X14551 and S81914.

Location/Qualifiers
1. 1368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 (bases 1 to 74371)
Kimmerly, W., Bondoc, M., Cheng, J., Connolly, K.S., Gunning
Davis. C.A., Kadner, K., Miguel, T., Pitluck, S., Pollard, M.
Rojeski, H., Subramanian, S. and Martin, C.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1330 ATGTGTCACTCTCGCAGCTGCCACCGACCATGACCATC 1368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
/product="DIF-2 protein"
/db_xref="PID:e1292739"
/db_xref="PID:93133089"
/translation="MCHRRSCHPPMTI"
a 362 c 343 t
                                                                                                                                                                                                                                                                                         /product="DIF-2 protein"
1295. .>1368
/gene="dif-2"
                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="6"
/map="p21.3"
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1330. .>1368
/gene="dif-2"
                                                                                                                                                                                                      /gene="dif-2"
<1. .>1294
                                                                                                                                                                                                                                            /gene="d1f-2"
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/gene="dif-2"
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Best Local Similarity 100.0%;
Matches 39; Conservative
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                1 (bases 1 to 215)
Bennett, A., Labavitch, J.M., Powell, A. and Stotz, H.
Bennett, A., Labavitch, J.M., Powell, A. and Stotz, H.
Blant inhibitors of fungal polygalacturonases and their use to control fungal disease
Patent: US 5569830-A 5 29-OCT-1996;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | :: : | |::: | :: : | |:: | 536 CCAGGTACTTTTGGGGATTCTTTTGGGGAGTGCGGGGA-G 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78 THYYTHINVSGADSKTVTDSYNASGISSSNGGTDGNRSGADSYGSSKTAMISRN-RIGKI 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  477 TCACAGTTAG-AAGGCGGCCGGGTGTTGCTGGAGGAAAGTGCTGAGGTCCAGAGCGTAGT 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    137 ANNAVDSRNMGDASVGSDKNTKKHAKNSADGKVGSKNNGDRNN-RYGTGTKSNVSNNCGG 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      926 CICCCCATITCTTCTTCTACTTTGCCGCAGTTCCAGGTGTCCTGCTTCCACCAGTCCCAC 867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1368)
Pietzsch,A., Buchler.C. and Schmitz,G.
Genomic organization, promoter cloning, and chromosomal localization of the Dif-2 gene
                                                                                                                                                                                                                                                              30-0CT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18 CNDKAKKDGNTTSSWTTDCCNRTWGVCDTDTTYRVNNDSGHNKYSSANYNYGGNNVGAAK 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-MAY-1998
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                                                  986 TAAACTTACGACCCACCACGAGACTTCATCCCAGCCGGGACGTCCTCCCCCACCCGAGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4
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98249769
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Homo sapiens dif-2 gene, promoter region.
Y16736
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Pred. No. 4.73e-06;
79; Mismatches 80
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                                                                                                                                                                                                                                 Sequence 5 from patent US 5569830.
128278
91819054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="unknown"
8 c 25 g
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                                                                                                                                                    1423 YYYYYYYYYYGTACCAA 1441
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                                                                                                                                                                                      866 AAGCTCAATAAATACCAA 848
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Pietzsch, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 3.3%;
Best Local Similarity 18.1%;
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                 Unclassified.
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dif-2 gene.
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Gaps

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Length 1368;

US-08-799-910-9.rge

source	174371 /organism="Homo sapiens" /db_xref="taxon:9606" /map="sq" /clone="11913" /chromosome="5"	repeat_region repeat_region repeat_region	/rpt_family="MER42" complement(1767818276) /rpt_family="Au" 1930519583 /rpt_family="Alu" 1931419948
repeat_region	/note="LBNL H175" 893. 1030 /rof familu-alu"		/note="(GTT)8" /rpt.type=tandem /rst.it_cmm
repeat_region	2255. 245. 7rot family	repeat_region	//pc_durt=6111. complement(19432022)
repeat_region	/.tpc_tammir_ Aid /.tpc_tammir_ Aid /.note==(GT)]=	repeat_region	/rpc_ramily="ALU" 2120521405. /t form:
	/rpt_type=tandem /rpt_unit=GT	repeat_region	//pc_ramily
misc_feature	.3828)	repeat_region	/ip/dminty_ Aid /2017
repeat_region	/note="65% & 69% protein identity GenPept:U22377" 3431. 3724		/rpt_type=tandem /rpt_unit=A
repeat_region	/rpt_family="Alu" 37073728	repeat_region	2232122457 /rpt_family="Alu"
	/note="(A)22" /rpt_type=tandem	repeat_region	complement(2263822981) /standard_name="possible repeat"
repeat_region	/rpt_unit=A 43664661	repeat_region	
repeat_region	/rpt_family="Alu" 53275602	repeat_region	2347323761 /rpt_family="Alu"
repeat_region	/rpt_family="Alu" 65866956	repeat_region	2374423767 /note="(A)24"
repeat_region	/rpt_family="L1" 66476684	•	/rpt_type=tandem /rpt_unit=A
	/note="(CA)19" /rpt_type=tandem	repeat_region	complement(2463924694)
repeat_region	/rpt_unit-CA 71137373	repeat_region	complement(2534925713) /rpt family="Alu"
	/rpt_family="Alu" complement(7830, .8185)	repeat_region	complement(2572726471)
	/standard_name="possible repeat" 8258 . 8503	repeat_region	27191
	/rpt_family="Alu"	repeat_region	7.174
	/rpt_family="Alu"	repeat_region	/10c_idiliy= Aid /2040 28066 ////
	/rpt_amily='MER42' Complement(10440 11015)		/note="(A)z/" /rpt_riype=tandem /rpt_riype=tandem
	/rpt_family="Alu"	repeat_region	28712. 20112.
	/rpt.com/rpt.alu= /rpt.com/rpt.alu= 12057_12085	misc_feature	3
	/note="(A29" /rot type=tangem	repeat_region	/BOCE GRAIL Z excellent exon, Ifame U. 289872917
repeat_region	/rpt_unit=A 1236512645	misc_feature	/ipc_idmiij_ Aid join(29485; 19559,29598; .29779) /note="95% identity Abstr.cid522 /cucc_il312)"
	/rpt_family="Alu" 1372713750	misc_feature	
	/note='(AC)12" /rpt_type=tandem	misc_feature	10.x1"
repeat_region	/ 15/2 unit-Ac 1378 11424 /rot familiar!	repeat_region	<pre>/note="GRAIL 2 excellent exon, frame 2" complement(3068230733)</pre>
repeat_region	/1/2-14475	misc_feature	/rpt_ramily="Mik" complement(3157331724)
repeat_region	complement(14906. 15259)	misc_feature	
repeat_region	1530015613 / // // // // // // // // // // // //	repeat_region	1100
repeat_region	1667]16690 /note="(T)20"	repeat_region	7.57
	/rpt_type=tandem /rpt_unit=T	repeat_region	32 <u>97733</u> 088 /rpt_family="MLT1"
	complement(1667516977) /rpt_family=Alu=	repeat_region	complement(3367033785) /rpt_family="Alu"
repeat_region	complement(1699317085)	misc_feature	complement(3402134144)

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/db_xxef-"PID:92305221"

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QLRAADESFKGVTFISPAHVTLPKSVDWRTKGAVTAVKDOGHGGSCWAFSSTGALEGO
HFRKGSVLYSLSEQNIVDCSTKYGNNGCNGCLMDNAFRYIKDNGGIDGEKSYBYFAID
DSCHFNKGYVGATGFTDIPGOBEKKMABNAFAYTVGPVSVALDSFSSTYFAID
DSCHFNKGYVGATGFTDIPGOBEKKMABNATVGPVSVALDSFSSEYFNID
DSCHFNKGYVGATGFTDIPGOBEKKMABNATVGPVSVALDSFSEYFYFAID
DSCHFNKGYVGATGFTDIPGOERKMABNATVGPVSVALDSFSSTYN
EPQCDAQNLDHGVLVVGFGTDESGEDYWLVKNSWGTTWGDKGFIKMLRNKENOCGIAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="phenylalanyl tRNA synthetase"
/db_xref="PID:92305222"
/translation="MLLTLRVQGARHWLKSTRCLASSAAPAKSPSSPPQLEVSGSTYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOGWTNVT PKILSYVGANKHLOTDHPLSIIRQRIVNY FYGAYRNQRGNPLFSVYDOWN
PVVTVQQNFDNLLIPADHVSRQKSDCYYINQOHLLRAHTTAHQVELISGGLDNFLVVG
EVYRRDEIDSTHYPVFHQADAVRLVTKDKLFERNPGLELFEETWSGTLADPKLILPHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SSWTKPNSPATRRAVKLMEHEMKHVLVGLTKDLFGPRIKYRHVDTYFPFTQPSWELEI
YEDDMALEVGGGIMKHEILQRSGYHQSIGYARGVGLERLAMVLEDIDDIRLFWNDS
GFLSQPSEKDLHNLFWKYRPTSHYPQCTNDLSFWLPQDIEVDAGFSPNDFYDLYRSVAG
DMYEQISLYDKFKHPKTGKSSVCFRIVYRHMERTLTQAEVNEIHKQIASASVDSFNVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster cysteine proteinase-1 (CP1) gene, complete cds, and phenylalanyl tRNA synthetase gene, partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ä
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Pred. No. 4.16e-04;
57; Mismatches 27; Indels
                                                                                                                                                                                                                 .2426,6476. .6690,6751. .7462)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of P[CaSpeR](50C)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="phenylalanyl tRNA synthetase"
| poin(8110. .9300,9370. .>9532)
| note="potential orf"
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                                                                                                                                                                                                                                                                                    'product="cysteine proteinase-1"
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             /gene="CP1"
872. 1000
/gene="CP1"
/number=1
                                                                                                     1001. .2309
/gene="CP1"
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/gene="CP1"
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/gene="CP1"
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Best Local Similarity 18.1%;
Matches 19; Conservative
                                                                                                                                                                                                                                      'gene="CP1"
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/gene="CP1"
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/gene="CP1"
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6751. .7707
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/gene="CP1"
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                                                                                                                                                                                                                 complement (37595. 37654)

/note="GRAIL 2 excellent exon, frame 0" complement (join (38063. 38218,38462. 38578,38741. 38995, 39071. 33205,39532. 39630,39935. 40048,40300. 44410, 44507);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryotae: mitochondrial eukaryotes; Metazoa; Arthropoda;
Tracheata; Hexapoda; Insecta; Pterygota; Diptera; Brachycera;
Muscomorpha: Ephydroidea; Drosophilidae; Drosophila.
1 (bases 4546 to 453)
Gray, Y. H., Tanaka, M.M. and Sved, J.A.
P-element-induced recombination in Drosophila melanogaster: hybrid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AF012089 10772 bp DNA INV 05-AUG-1997 Drosophila melanogaster cysteine proteinase-1 (CP1) gene, complete cds, and phenylalanyl tRNA synthetase gene, partial cds. AF012089 92305220
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Submitted

(30-JUN-1997) School of Biological Sciences, University

of Sydney, Biology Al2, Sydney University, NSW 2006, Australia

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     336 GGACGCCCTAACGCCGCATCCCTGGCGCCCACCCCTGTGTCCCCCCGTCCTCGACCCCTT 395
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join(872. 1000,2310. .2426,6476. .6690,6751. .7707)
/gene="CP1"
/product="cysteine protease"
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                                                                                                                                                                                                                                                                                                                                                                       /standard_name="histidyl-tRNA synthetase"
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complement(38462. 38578)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 3.1%; Score 38; DB 26; Length 74371; Best Local Similarity 16.7%; Pred. No. 1.38e-04; Matches 15; Conservative 49; Mismatches 26; Indels 0
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Genetics 144 (4), 1601-1610 (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             annotations omitted.
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/translation-"MLLTLRVQGARHWLKSTRCLASSAAPAKSPSSPPQLEVSGSTYA
TDGGWTVYTPAKTLSYVGANKHLQTDHPLSIRQDKIVNYFYGARYRQKGBHESYYDQMN
PVVTVQONFDNLLIPADHVSRQKSDCYINQHLLRAHTTAHQVELISGGLDFLVVG
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DMVEQISLVDKFKHPKTGKSSVCFRIYYRHMERTLTQPAEVEHEHKGIARARSVEFNVO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACU05369 74371 bp DNA PRI 01-AUG-1998
Homo sapiens chromosome 5, BAC clone 119j3 (LBNL H175), complete
AC005369
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                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
Bukaryota, Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 7431)
Kimmerly,W., Bondoc,M., Cheng,J., Connolly,K.S., Gunning,K.M., Radner,K., Miguel,T., Miller,C., Pitluck,S., Pollard,M.,
Sejeski,H., Subramanian,S. and Martin,C.H.
Sequencing of human chromosome 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Large Scale Sequence Analysis and Annotation with the Sequence Comparison Analysis (SCAN) System
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Minmerly, W., Bondoc, M., Cheng, J., Connolly, K.S., Gunning, K.M., Bavis, C.A., Kadner, K., Miguel, T., Pitluck, S., Pollard, M., Brojeski, H., Subramanian, S. and Martin, C.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (01-AGG-1998) Human Genome Center, DOE Joint Genome Institute, Lawrence Berkeley National Laboratory, MS 74-157, Berkeley, CA 94720, U.S.A. Sequence submitted by:

DOE Joint Genome Institute.

Location/Qualifiers
                                                                                                                                                                                                                                                           Length 10772;
                                                                                                                                                                                               158 others
                                                                                                                                                                                                                                                         Score 35; DB 18; Length 107
Pred. No. 3.65e-03;
55; Mismatches 28; Indels
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/db_xref="taxon:9606"
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/rpt_family="Alu"
2295. .2438
/rpt_family="Alu"
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/note="(GT)21"
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Ricke, D.O.
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Best Local Similarity 19.0%;
Matches 20; Conservative
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/translation="MTAVALDFLLALLAVAQANSFADVVMEEWHTFKLEHRKNVQDET
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DSCHPNRGTVGAPGFTDIPGOEDEKMABANATVGPVSVALDGRSGFYN
EPOCDAONLDHGVLVVGFGTDESGEDYMLVKNSWGTTWGDKGFIKMLRNKENQCGIAS
                                                                                                                                                                  Gray,Y.H., Tanaka,M.M. and Sved,J.A.
P-element-induced recombination in Drosophila melanogaster: hybrid
                                                                                                                                                                                                                                                                                                                                                           Unpublished
3 (bases I to 10772)
Gray, Y. H.M., Sved, J.A., Preston, C.R. and Engels, M.R.
Direct Submission
Submitted (30-JUN-1997) School of Biological Sciences, University of Sydney, Biology Al2, Sydney University, NSW 2006, Australia
Location/Qualifiers
                                                                                                                                                                                                                                                                                               Gray, Y.H.M., Sved, J.A., Preston, C.R. and Engels, W.R. Structure of the cysteine proteinase (CP1) gene of Drosophila melanogaster and associated mutational effects
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
join(872. .1000,2310. .2426,6476. .6690,6751. .7707)
/gene="CP1"
                                                                                Eukaryotae; mitochondrial eukaryotes; Metazoa; Arthropoda;
Tracheata; Hexapoda; Insecta; Pterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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/gene="CP1"
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/product="phenylalanyl tRNA synthetase"

join(8110. .9900,9370. .>9532)
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872. .7707
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                                                            Drosophila melanogaster
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6476. .6690
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/gene="CP1"
872. .1000
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2310. .2426
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4546. .4553
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36901. 37164

36901. 37164

/standaname="STSG-9983"

/db_xref="dbSTS:G26554"

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/note="GRAIL 2 excellent exon, frame 0"

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complement(3010(38063. 38218,38462. 38578,38741. 38995,

39071. 39205,39532. 39630,39935. 40048,40300. 40410,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /rpt_family="Alu"
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join(29485. .29559, 29598. .29779)
/note="95% identity dbsTs:G14522 (SHGC-11312)"
29495. .2996me="A1027942"
/note="100% identity EST ov84a10.x1"
/note="GNAIL 2 excellent exon, frame 2"
/note=mGRAIL 2 excellent exon, frame 2"
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/rpt_family="MRR"
                                                                                                                                                                                                                                                                                                                                                                                            28040. .28056

// note="(A)27"

/rpt_rype=tandem

/rpt_unit=A

28112. .28930

/rpt_family="MER20"

/rote="GRAIL 2 excellent exon, frame 0"

28987. .29214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complement (31573. 31724)

foote-"GRAIL 2 excellent exon, frame 1"

complement (3159. 32232)

foote-"GRAIL 2 excellent exon, frame 2"

32388. 32488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         frame 2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /rpt_family="Alu"
36901. 37222
/note="100% identity EST ou55c09.x1"
46b_xref="dbsSr:Alo25011"
16901. 371f4
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23022. .23326
/rpt_family="Alu"
23473. .23761
23744. .23767
/note="(A)24"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(34021. 34144)
/note="GRAIL 2 excellent exon,
complement(35238. 35331)
/note="GRAIL 2 excellent exon,
36392. 36663
                                                                                                                                                                                                                                   /rpt_family="MER42"
complement(25349. .25713)
/rpt_family="Alu"
complement(25727. .2647''
                                                                                                                                                                                                                                                                                               rpt_family="Alu"
7191. .2747
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complement(33670, .33785)
/rpt_family="Alu"
                                                         22321. .22457
/rpt_family="Alu"
complement(22638. .22981)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /rpt_family="MLT1"
32617. 32908
/rpt_family="Alu"
32977. 33088
                                                                                                                                                                                                                                                                                                                                                                           rpt_family="Alu"
8040. .28066
                                                                                                                                                                                                                                                                                                                                                   .pt_family="Alu"
774. .28057
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                              /rpt_type=tandem
/rpt_unit=A
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Join(3246. .3410.3721. .3828)
/standard_name="RLF"
/note=="658 & 698 protein identity GenPept:U22377"
                                                                                                                                                                                                                                                                                             7113. 7373
/rpt_family="Alu"
complement(7830. .8185)
/stendard_name="possible repeat"
8258. .8503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mplement(14906. .15259)
tandard_name="possible repeat"
300. .15613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(16993. 17085)
/rpt_family="MER42"
complement(17678. 18276)
/rpt_family="Alu"
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/rpt_family="Alu"
1950. 19250.
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pmplement(9740. .9845)
pt_family="MER42"
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12057. 12085
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/rpt_type=tandem
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/rpt_family="Alu"
3707. .3728
/note="(A)22"
/rpt_type=tandem
/rpt_unit=A
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21736. .22035
/rpt_family="Alu"
                                                                                                                                        4366. .4661
/rpt_family-"Alu"
5327. .5602
/rpt_family-"Alu"
6586. .6956
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671. .16690
ote="(T)20"
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rpt_family="Alu"
3727. .13750
note="(AC)12"
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pt_family-"Alu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pt_family-"Alu"
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6647. .6684
/note="(CA)19"
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/rpt_unit=CA
                                                                                                                                                                                                                                                                                                                                                                     t_family-"Alu"
0. .9387
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L_family="L1"
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rpt_unit=T
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783. .14024
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           misc_feature
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Gaps

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Length 192,

30-JUN-1997

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Redeveloped chromosome 4 markers for scoring on oligonucleotide arrays. Designed and developed at the Stanford Human Genome Center on sequences previously developed as STSs at the Stanford Human Genome Center or the Whitehead Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Initial incubation: 94 degrees C for 90 seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Richard M. Myers
Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, M-344, Stanford, CA 94305, USA
Tal: 4157259687
Fax: 4157259689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94 degrees C for 15 s
62 degrees C for 23 s
72 degrees C for 30 s,
30
Perkin Elmer 9600
                                                                                                                                                                                                                                                                                                                            G34020 408 bp DNA STS human STS SHGC-51059, sequence tagged site. G34020 91227324 STS; STS sequence; primer; sequence tagged site.
                                                                                                                                                               40 TGCAGGATGGTCATGGTGGGGTGGGAACTGCGGAAGTGACACAT 83
                                                                                                                                                                                               Score 34; DB 30;
Pred. No. 1.06e-02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25 ng
each 1 uM
each 200 uM
0.05 units/ul
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STS size: 128
PCR Profile:
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/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.5 mM
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20 mM
8.3
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a 89 c 124 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: myers@shgc.stanford.edu
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Total Vol:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Annealing:
Polymerization:
PCR Cycles:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thermal Cycler:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Denaturation:
                                                    Query Match 2.8%;
Best Local Similarity 88.6%;
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 408)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Myers, R.M.
Unpublished (1997)
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Tris-HCl:
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primer_bind
BASE COUNT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human.
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                                                                                                                                                                                                                                                                                                          18
                                                                                                                                                                                                                                                                                                                                                               DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                             KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
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     DRIGIN
                                                                                                                                                                                                                            g,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HUM4S1251 192 bp DNA STS 10-AUG-1993
Human Chromosome 4 (clone p4-1696) STS4-1251, sequence tagged site.
L17191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           oligonuclectide,
200 micro-M dMTPs, 0.25 U Taq polymerase (Cetus) in 10 micro-l of
200 micro-M dMTPs, 0.25 U Taq polymerase (Cetus) in 10 micro-l of
30 mM KCl-20 mM Tris-HCl, pH 8.3 (at room temp), 2.5 mM MgCl-2.
Thermocycler: PE 9600
PCR Profile: Initial denaturation: 94 degrees C for 1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seconds Annealing:
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40503. .40661,41868. .41972,42103. .42225,42492. .42569,
44379. .44507))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15996 CY-YSYKYYWSMSYCTCTSWGWRWMWSKGRSWMYASRSGCSCSCSMCMMCRCSCM-SMKM 16053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 192) (base
                                                                                                                                                                                                                                                                                                                                                                                            Db 15936 KRGWGYRSWKKYRCAMWMTCKSSKCWCWSYRMRMKCYSCSYCYCSSGKKYWCRCSMYWYT 15995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16054 WWWTTTTTKTRTWTTTWKWRKAGASASRGK-SKCRCMSYGKKSTCKM-KMTCYYGMYSWC 16111
                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Stanford University
855 California Avenue
Palo Alto, CA 94304, USA
Palo Alto, CA 94304, USA
Primer A: TTCGTCCAGGATGGTCATGGTGG
Primer B: AGCCTGGGGGTACAAGACCAAAAC
PCR Components: 25 ng of human genomic DNA, 10 pmol of each
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Denaturation: 94 degrees C for 15 seconds An 62 degrees C for 23 seconds Polymerization: 72 degrees C for 3.5 minutes PCR Cycles: 30 Final extension: 72 degrees C for 3.5 minutes.
                       44379. .44507))
/standard_name="histidyl-tRNA synthetase"
/note="78%-100% protein identity GenPept:U18937"
complement(38069. .38215)
/note="GRAIL 2 excellent exon, frame 0"
complement(38462. .38578)
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..
                                                                                                                                                                                                                                                                                Length 74371;
                                                                                                                                                                                                                                                                             Score 36; DB 26; Length 743
Pred. No. 1.24e-03;
93; Mismatches 63; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g306334
STS; STS sequence; primer; sequence tagged site.
Homo sapiens DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted by: Human Genome Mapping Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21
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/db_xref="taxon:9606"
36. 177
36. 58
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Best Local Similarity 15.8%;
Matches 30; Conservative
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and Deeg, M.A.
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Mus musculus
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C.C.Query,
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A common RNA recognition motif identified within a defined UI :
blinding domain of the 70K UI snRNP protein
CELL 57 (1), 89-101 (1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71 NNVGAAKTHYYTHTNVSGADSKTVTDSYNASGISSSNGGIDGNRSGADSYGSSKTAMTSR 130
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                                                                                                                                     30-OCT-1996
                            Gaps
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Bennett, A., Labavitch, J.M., Powell, A. and Stotz, H.
Plant inhibitors of fungal polygalacturonases and their use
control fungal disease
Patent: US 5569830-A 5 29-OCT-1996;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein mRNA,
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Query, C.C., Bentley, R.C. and Keene, J.D.
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Length 408;
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                                                                                                                                                                                                                                                                                                                                                                                               Score 33; DB 21; Length 215
Pred. No. 3.04e-02;
79; Mismatches 101; Indels
 Score 34; DB 30; Length 408
Pred. No. 1.06e-02;
0; Mismatches 5; Indels
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Human U1 small nuclear ribonucleoprotein 70 kd
complete cds.
M22636
                                                       84 TGCAGGATGGTCATGGTGGGGTGGGAACTGCGGAAGTGACACAT 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human placenta and endothelium, cDNA to mRNA
Homo sapiens
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                                                                                                                                   128278 215 bp DNA
Sequence 5 from patent US 5569830.
128278
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                                                                                                                                                                                                                                                                                                                                       /organism="unknown"
8 c 25 a
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Best Local Similarity 12.2%;
Matches 25; Conservative
  2.8%;
Local Similarity 88.6%;
les 39; Conservative
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Direct Submission
Submitted (24-FEB-1998) Pathobiology, Univ. of Washington, Room 305
Raitt Hall/Box 353410, Seattle, WA 98195, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                               YKHADGKKIDGRRVLVDVERGRTVKGWRPRRLGGGLGGTRRGGADVNIRHSGRDDTSR
YDERGSPLPHRDRDRDRERRERSRERDKERERRSRSRSBRRRERSRRKERERRK
YDERRGSPLPHRDRDRDRRERERRERSRERDKREERRR
YDERRGGGDMAPPSEAGDAPPDGPPGE
LGPDGPPGPEERGRARDRERERRRDRDRDRDRDREHKRGERGSERGRDE
RGGGGGDNGLEGLGNDSRDWYMESEGGDGYLAPENGYLMEAAPE"
                                                                                                                                                                                                                                                                                     /db_xref="PID:g337447"
/translation="MTOFLPPNLLALFAPRDPIPYLPPLEKLPHEKHHNOPYCGIAPY
IREFEDPRDAPPPTRAETREERWERKRREKIERRQGEVETELKWWDPHNDPNAQGDAF
KTLFVARVNYDTTESKLRREFEVYGPIKRIHWYSKRSGKPRGYAFIEYEHERDMHSA
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LeBoeuf, R.C., Caldwell, M., Guo, Y., Metz, C., Davitz, M.A., Olson, L.K.
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LeBoeuf,R.C., Caldwell,M., Guo,Y., Metz,C., Davitz,M.A., Olson,L.K.
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(Gpld1)
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proteins in the presence of detergent"
/note="GPI-PLD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus glycosylphosphatidylinositol-specific phospholipase | procursor (Gpidi) mRNA, complete cds. AF050666 g2984690
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                                                                                                                                                                 /note="small ribonucleoprotein 70 kd protein mRNA"
172. .1485
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                                                                                                                                                                                                                                          /note="small ribonucleoprotein 70 kd protein"
                                                                                                  49. 81
/note="type C retrovirus p30gag-like region"
172. .1630
/partial
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Pred. No. 2.39e-01;
0; Mismatches 4; Indels
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/db_xref="taxon:10090"
/chromosome="13"
Location/Qualiflers
1. 1662
/organism="Homo sapiens"
/db_xref="taxon:9606"
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/cell_line="alpha-rc6"
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/gene="Gpld1"
271. .2784
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Best Local Similarity 89.7%;
Matches 35; Conservative
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                                / ADD_XTOTE_PAGE_DEFORMSSILLILPLECSKSSSCGLSTHVEIGHRALEFLRLQD
/ ADD_XTOTE_PAGE_DEFORMSSILLILPLECSKSSSCGLSTHVEIGHRALEFLRLQD
GRINYREALILEHODAYQAGTVFDAPYSICKRAYHWEIGHRAPELRAPELBERDDD
GRINYREALILEHODAYQAGTYFDAPYSICKRAYHWEIGHRAPELRAFGDFG
GROVLSQFEFNYREALILEHODAYGAGTYFDAFASAGTE
NYPLAWERDTERUNAFLEGTTSHNAVADLARITYGRYFTRAFASAGTESTHYRE
RYSTRYSTKSFPELVBOPODDYFLGGLODAFWSTNIYRILSTERDENGTSDCNLPE
RAYSKLYSTYSTKSFPELVBOPODDYFLGGLODAFWSTNIYRILSTERDENGTSDCNLPE
NYPMYQTLERNHTLSGSRVOKNDFHRALTMFISRD RKNLNYTBRGVFYSTGSWARPE
SVTPMYQTLERNLRHALGSSGVRNLNHVSSPSASYTLSVPYARLGWVHTSADLNODGH
GDLVVGAPOYSHPGRFOIGRYT IYGNDLGLPPIDTBLANGSTLEGFOPSGRRGSALA
VLDFNQDGLPDLAVGAPSSGGLIYNGSVYYYTSGSQCRLSSSPWYTISCKDTYCNL
GWTLLATDAAGGSRHDLYISSPFAPGGRROKGIVATFYSHPRRNDKELLTLEEADWKV
NGFEDFSWFGYSLHGVTVARRSLLLIGSPTKNUVSTRARSSHKKNOFERSIGKVYGYF
LPNROSTITISGBAMGKLGTSLSSGYVRWYGTLTQVLLUGBPTHDDVSKMAFLTMLL
HQGGATRWYELLAPERTQPALLSTFSGDFRFSRFGSVLHITDLDDDGLDBIIMAAPLRI
TDVTSGLLGGEDGRYYIYUGDMTGKCKSWMTPCPEERRAQVVLTSPEASSRFG
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/db_xref="PiD:gl134970"
/tb_xref="PiD:gl134970"
/tb_xref="PiD:gl134970"
/db_xref="PiD:gl134970"
/translation="VFMHFYUCLQAQVTVQSPPNFTQHVREQSLVTDQLSRRLVRTY
QLYSRTSGRWYQILDNKXIRAMAEDGDVHAKLIVFTDTFGSRVRIKGAATGFYICMNK
KGKLIGKSNGKGKDCVFTEIVLENNYTALQNAKYEGWYMAFTRKGRPRKGSKTRQHOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGU41467 800 bp mRNA VRT 02-APR-1996
Gallus gallus fibroblast growth factor 8 FGF8 mRNA, partial cds.
U41467
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Vertebrata; Archosauria; Aves; Neognathae; Galliformes;
Phasianidae; Phasianinae; Gallus.
1 (bases 1 to 800)
Crossley, P. H., Minowada, G., MacArthur, C.A. and Martin, G.R.
Roles for FGF8 in the induction, initiation, and maintenance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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/clone_lib="E10 embryonic chick brain cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (27-NOV-1995) Philip H. Crossley, Anatomy, UCSF, Parnassus, San Francisco, CA 94143-045, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="glycosylphosphatidylinositol-specific
  'product-"glycosylphosphatidylinositol-specific
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Pred. No. 2.39e-01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches 12; Indels
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/organism="Gallus gallus"
/db_xref="taxon:9031"
/dev_stage="embryo"
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                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="Gpld1"
                                                                                                                                                                                                                                                                                                                                                                                                  /gene="Gpld1"
340. .2781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     phospholipase
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Best Local Similarity 78.2%;
Matches 43; Conservative
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RFFVNFVVGGGGGADVAFHFNPRFDGWDKVVFNSQQDGKWGNEEKKRSMPFRRAPAFE
LVIMYLDEBIKKVVNKGDPFYEEGHRIPVQLVTHLQVDGDLTLQSINTIGGQPARSPGP
MPPGTPGPGKHNQQPCNLPCMEGAPTFNPPVPFXTRLQGGLVARRTIVIKGYVPPSG
KSLVINFKVGSSGDVALHINPRLTEGIVVRNSYLNGKWGAEERKSSFNFFAPGQYFDL
SIRCGLDRFKVYANGQHLFDFSHRLSNFQGVDTLEIQGDVTLSYVQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product-"L-36 lactose binding protein"
/db_xref-"PID:9623346"
/translation-"MAFVPAPGYQPTYNPTLPYYKPIPGGLRVGMSVYIQGVANEHMK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (18-MAY-1994) E.J. O'Keefe, University of North Carolina, 137 NCMH, Dept of Dermatology, CB7600, Chapel Hill, NC 27514, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vertebrata; Eutheria; Artiodactyla; Suiformes; Suina; Suidae; Sus. I (bases 1 to 1125)
Chiu,M.E., Parry,D.A., Feldman,S.R., Klapper,D.G. and O'Keefe,E.J. An adherens junction protein is a member of the family of
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                                                          Length 800;
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/cell_type="keratinocyte"
/clone_lib="pig toungue cDNA"
49. .1020
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                                                                                                                                                                                                                                                           SSL36LBP 1125 bp RNA MAM
S.scrofa mRNA for L-36 lactose binding lectin.
X79303
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                                                                                 1.76e+00;
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Pred. No. 1.76e+00;
                                                             DB 20;
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                                                                                                                                                                                                                                                                                                                                                                    1-361bp gene; lactose-binding lectin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism-"Sus scrofa"
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Bos taurus retina cDNA to mRNA.
                                                                                   Pred. No.
                                                             Score 29;
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/dev_stage="adult"
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1. .1125
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ь
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49. .1020
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/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lactose-binding lectins
                                                          2.4%;
ilarity 74.6%;
Conservative
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Best Local Similarity 89.2%;
Matches 33; Conservative
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Direct Submission
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REFERENCE AUTHORS TITLE

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/db_xref-"PID: 92505940"
/db_xref-"SPTREMBL: 035593"
/translation-"MORLLERGGGMEGLARPPTDAPAVDTAEQUYISSLALLKMLKHG
RAGVPHEVMGLMLGEFVDDYTVRVIDVFAMPQSGTGVSVEAVDPVFQAKMLDMLKQTG
RPEMYVGWYBKBRPGFGCWLGSGVDINTOQSFEALSERAVAVVDDPIOSYKGKVVIDAFR
LINANMMVLGHEPRQTISNLGHLNKPSIQALIHGLNRHYYSITINYRKNELEQKMLLN
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QDPKRHLEEHVDVLMTSNIVQCLAAMLDTVVFK"
270 c 349 g 407 t
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Eukaryotae; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea;
Pipidae; Xenopodinae; Xenopus;
I (bases 1 to 1811)
Cordes, V.C., Reidenbach, S., Rackwitz, H.R. and Franke, W.W.
Identification of protein p270/Tpr as a constitutive component of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              XLUG9669 1811 bp mRNA VRT 26-FEB-1997
Xenopus laevis nuclear pore complex-associated protein TPR (tpr)
mRNA, partial cds.
                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

(Dases 1 to 1479)

Penney,M., Wilkinson,C., Wallace,M., Javerzat,J.P., Ferrell,K., Seeger,M., Dublal,W., McRay,S., Allshire,R. and Gordon,C.
The pad1(+) gene encodes a subunit of the 26 S proteasome in fission yeast
J. Blol. Chem. 273 (37), 23938-23945 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (08-MAY-1997) C. Gordon, MRC Human Genetics Unit,
Developmental Genetics, Western General Hospital, Crewe Road,
Edinburgh EH4 2XU, UK
Location/Qualifiers
                                                                                                                                                                                                  26S proteasome; non-ATPase subunit; proteolysis; regulatory
                                                   MM26SPROT 1479 bp mRNA ROD 10-SEF
Mus musculus mRNA for 26S proteasome non-ATPase subunit.
Y13071
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Pred. No. 1.76e+00;
0; Mismatches 5.
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/product="26S proteasome,
/db_xref="PID:e352083"
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/organism="Mus musculus"
/db_xref="taxon:10090"
/dev_stage="adult"
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/gene-"PAD1"
237. .1166
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/gene="PAD1"
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2.4%;
Best Local Similarity 87.2%;
Matches 34; Conservative
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TITLE
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/db_xref="PiD: 9156706"
/tanslation="RFEELCADLFRSTMDPVEKALRDAKMDKAQVHDIVLVGGSTRIP
KVQKILLSDFFSGKERSINPDEAVAYGAAVQAAILGGDKSERAVGDLLLDVAPLSIG
IETAGGVMTALIKRWTTIPTKTSQTFTTYSDNQPGVLIQVYEGERAMTKDNNLLGKFE
LSGIPPAPRACYPQIEVTFDIDANGILMYSAQDKSTGRQNKTITTNDKGRLSKDETERM
LSGIPPAPRACYPQIEVTFDIDANGILMYSAQDKSTGRQNKTITTNDKGRLSKDETERM
VSGARKYRADDEAQGNRIAAANMAGLISYAFANKQTIERM
TVRWLDGNQTAEKDEFEHRQKELESVCNPIITKLYQSAGGMPGGMPGGAPGGAAGGGS
                             Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Artiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinea; Box 1 to 1266)

Yang, 2. and Wensel, T.G.
Wolecular cloning and functional expression of cDNA encoding a mammalian inorganic pyrophosphatase
J. Biol. Chem. 267, 24641-24647 (1992)
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Birofilaria immitis 70 kDa heat shock protein homologue (hsp 70)
M95648
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Dirofilaria immitis adult cDNA to mRNA.
Dirofilaria immitis

Dirofilaria immitis

Dirofilaria immitis

Eukaryotes; Metazoa; Nematoda;

Secernentea; Spiruria; Spirurida; Spirurina; Filarioidea;

Onchocercidae; Dirofilaria.

E 1 (bases 1 to 1294)

S Culpepper, 7.A., Friedman, L. and Dale, B.

Molecular cloning and characterization of a Dirofilaria immit cDNA encoding an HSP 70 homologue

Unpublished (1992)
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Pred. No. 1.76e+00;
0; Mismatches 5; Indels
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Pred. No. 1.76e+00;
0; Mismatches 5;
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/organism="Bos taurus"
/db_xref="taxon:9913"
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239 c 300 g
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Best Local Similarity 87.2%;
itches 34; Conservative
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Best Local Similarity 87.2%;
Matches 34; Conservative
      Bos taurus
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ORIGIN
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MEDLINE
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ORGANISM

ACCESSION KEYWORDS

2 ò REFERENCE AUTHORS TITLE

JOURNAL

FEATURES

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Gaps

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/codon_start=1
/db_xref="PiD:9520932"
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/db_xref-"PID:g1668029

/db_xref-
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/gene="fpa2"
/note="SRP1-like; similar to the product of the fpa1 gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (14-FEB-1994) Rolf Mueller, Institut fuer
Molekularbiologie und Tumorforschung (IMT), Emil-Mannkopff-Strasse
2, Marburg, 35037, Germany
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 1941)
Wick,M., Burger,C., Brusselbach,S., Lucibello,F.C. and Muller,R. A novel member of human tissue inhibitor of metalloproteinases stamulation, differentiation, and senescence J. Biol. Chem. 269 (29), 18953-18960 (1994)
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Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ECLWIDMLSNFGYPGYQSKHYACIRQKGGYCSWYRGWAPPXKSIINAIDP"
496 c 437 g 499 t 3 others
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Pred. No. 1.76e+00;
0; Mismatches 6; Indels
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Pred. No. 1.76e+00;
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/db_xref="taxon:9606"
/clone="30-13 (mig-5)"
/cell_type="Fibroblast"
/cell_line="WI-38"
                                                                                                                                                                                                                                                                                                                                                                                            170 g
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42. .674
                                                                                                                                          /codon_start=
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/gene="fpa2"
a 166 c
                                     /gene="fpa2"
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Mueller, R.
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Best Local Similarity 85.4%;
Matches 35; Conservative
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Best Local Similarity 87.2%;
Matches 34; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product-"Tpr"
/db_xref-"PID:g1850344"
/db_xref-"PID:g1850344"
/translation-"VQPTQQSHATIESPTQETPVEIVQSSPVERPTTSSTFGTYSATP
S\SINEREEEDSTIETPEQIADDTDQQRTKKRKEEDIEEKTETEAVINTEDALHI
LTQCSNWEFPLEEEETYESPIOTSQVIESQAPEQLQNVOSTQOSLQDPPPKKTHULVIV
ISDEENEDEQEGYEEEEQEDEEEDEDDAGIGEGDDSNEETGSADGNEDYEGDDAEEAD
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PPSSSIADTSSKPKPRWLQPQPGRPFKRSRGGSDFRGRGGINRSNI*
427 c 427 q 380 t
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POSPRRQAPPRALTIAPPQELGPPPAQRIPVNRRQSVGRGLQLFPGVGRQQHFPDEE
DRTVBSTPTLVVPHTTDGFAET HSPQVAGVRFRFGPEDMPQASSSHSDLGQLASQ
GGLGMYDTPLFAHEEESGGRSVPTTPLQVAAPVSVFAENPAADTSDHASQSVPMYTT
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Dictyostelium discoideum
Dictyostelium discoideum
Lukaryotae; Dictyostelilda; Dictyostelium.
L (bases 1 to 1840)
West, C.M., Kozarov, E. and Teng-umnuay, P.
The cytosolic glycoprotein FP21 of Dictyostelium discoideum is encoded by two genes resulting in a polymorphism at a single amino gene 200 (1-2), 1-10 (1997)
                                                                                                                              Cordes V.C., Hunzicker, A. anu trummy.

Direct Submission
Submitted (06-SEP-1996) Cell Biology/0110, German Cancer Research
Center, INF 280, Heidelberg 69120, Germany
Location/Qualifiers
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use nuclear pore complex-attached intranuclear filaments
3. Cell Biol. 136 (3), 515-529 (1997)
97177132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complex-associated protein;
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/tissue_type="kidney"
/clone_lb="Uni-ZAPTMXR library, Stratagene"
1. .1678
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Pred. No. 1.76e+00;
0; Mismatches 11; Indels
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/strain-"Ax3"
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West,M.C., Kozarov,E. and Teng-umnuay,P.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note-"nuclear pore complex-a
translocated promotor region"
/codon_start=2
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1061. .1703
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Best Local Similarity 78.4%;
Matches 40; Conservative
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TITLE
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윱 ò

to specify

30

RESULT

셤 ò DEFINITION ACCESSION

ORGANISM

NID KEYWORDS SOURCE

REFERENCE AUTHORS

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/product="stem cell leukemia protein"
/db_xref="PID:92921801"
/db_xref="PID:92
                                                               Eukaryota: Metazoa: Chordata; Vertebrata: Actinopterygil;
Neopterygil: Teleostel: Euteleostel: Ostarlophysi; Cypriniformes;
Opprinoidea: Cyprinidae: Rasborinae; Danio.
1 (bases 1 to 2873)
Liao.E.C., Paw.B.H., Oates, A.C., Pratt, S.J., Postlethwait, J.H. and
                                                                                                                                                                                                                                                                                                                                                                                                       Liao, E.C., Paw, B.H., Oates, A.C., Pratt, S.J., Postlethwait, J.H. and
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Eutheria; Artiodactyla; Suiformes; Suina; Suidae; Sus.
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/gene="tal-1"
/note="basic helix-loop-helix transcription factor; SCL"
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Submitted (28-FEB-1997) W. Gebhard, Klinikum Grosshadern, HNO
Forschung, Marchioninistr. 15, 81377 Wuenchen, 81377, FRG
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heavy-chain H2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (30-JAN-1998) Hematology/Oncology, Harvard Medical
School, 300 Longwood Avenue, Boston, MA 02115, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cell_type="hematopoletic progenitors; angioblasts" 1. 2873 297. .1287
                                                                                                                                                                                                                   SCL/Tal-1 transcription factor acts downstream of cloche
hematopoietic and vascular progenitors in zebrafish
Genes Dev. 12 (5), 621-626 (1998)
98167906
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Pred. No. 1.76e+00;
0; Mismatches 10; Indels
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Secrofa mRNA for inter-alpha-inhibitor
Y11545
g1915953
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/organism="Danio rerio"
/db_xref="taxon:7955"
/chromosome="LG XXII"
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/organism="Sus scrofa"
/db_xref="taxon:9823"
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Vertebrata; Eutheria;
1 (bases 1 to 3042)
Gebhard,W.
                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 2873)
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Best Local Similarity 79.6%;
Matches 39; Conservative
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2 (bases 1 to 3042)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="allancoinase"
/db_xref="PlD:9458126"
/db_xref="PlD:9458126"
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/tb_xref="PlD:945805KI"
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SVLAMPHYTSGAKLLDVGDLVVMAGIIDPHVHVNEPGRTDWEGYRTATLAAAGGI
TAIVDMPLNSLPPTTSYTNFHTKLQAAKRQCYVDVAFWGGVIPDNQVELIPMLQAGVA
GFKCFLINSGVPEFPHVSVTDLHTAMSELQGTNSVLLFHAELEIAKPAPEIGDSTLYO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (13-NOV-1993) Reddy J.K., Northwestern University Medical School, Pathology, 303 E. Chicago Ave., Chicago, IL 60611-3008, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TFLDSRPDDWEIAAVQLVADLCQQYKVRCHIVHLSSAQSLTIIRKAKEAGAPLTVETT
HHYLSLSSEHIPPGATYFKCCPPVRGHRNKEALWNALLQGHIDWVVSDHSPCTPDLKL
LKEGDYMKAMGGISSLQFGLPLFWTSRTRGFSLTDVSQLLSSNTAKLGGLGIYKEPL
KWYMALIWSSGILTKSFKMHFITRISSPHIWDSFFKEKSWLLLFEGLLFISKGSM
LPNOLENIEYTLWSFKYRVHPPIRKNLPHI"
478 c 460 g 557 t
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Danio rerio stem cell leukemia protein (tal-1) mRNA, complete cds.
AF045432
g2921800
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Vertebrata; Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea;
                                                                                                                                                       RCALN 2116 bp mRNA VRT 22-JUN-1994
Rana catesbeiana allantoinase (ALN) mRNA, complete cds.
U03471
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/function="catabolizes allantoin to alantoic acid"
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Pred. No. 1.76e+00;
0; Mismatches 7; Indels
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J. Biol. Chem. 269, 12269-12276 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism-"Rana catesbelana"
/db_xref-"taxon:8400"
/clone-"FALN"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="liver"
/dev_stage="adult"
64. .1518
64. .1518
64. .1518
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Reddy, J.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene-"ALN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 2.4%;
Best Local Similarity 83.7%;
Matches 36; Conservative
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                                                                                                                                                                                                                                                                                                                                                                        Rana catesbeiana
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ranidae; Rana.
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                                                                                                                                                                                                                                                                                                                                        bullfrog
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source

PEATURES

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MEDLINE REFERENCE AUTHORS

JOURNAL

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LOCUS DEFINITION ACCESSION NID

KEYWORDS

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RESULT

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BASE COUNT ORIGIN

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Gaps

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DIFVASFEISFEEOLSMLDSVHLKVRLSKATELVDRHLQSILVAEKTTQKVEGQLSKS
QKEFLLRQQMRAIKEELGDNDDDEDDVAALERKWQNAGMPANIWKHAQREMRRLRKMO
POQPOTSSRAYLELLADLPWQKVSEERELDLRVAKEELDOBHYGLTKVKORITEYLA
VRKLKPDARGVULCFVGPPGVGKTSLASSIAKANRKFIRISGGWDEADIRGHRRY
YIGSWFGRLDGLKRYSVSNHVMLLDEIDKTGSDVRCDPASALLEVLDPEQNKAFNDH
YLNVPFDLSKVIFVATANRMQPIPPPLLDRMEIIELPGYTPEEKLKIAMKHLIPRVLE
OHGLSTTNLQIPEAMVKLVIERYTREAGVRNLERNLAALARAAAVKVAEQVKTLRLGK
                                                                                                                                                                                                         EIOPTTTLLDSRLADGGEVEMEVIPWEHDISNTYENPSPMIVDEAMLEKVLGPPRFD
DREAADRVASPGYSVGLVMTSVGGEVOFVEMTAMVGKGDLHLTGGLGDVIKESAOLAL
TWYRARAADLNLSPTSDITULLESRDIHIHFPAGAVPKDGPSAGVTLYTALVSLFSNRK
VRADTAMTGERTLGLYLLPVGGVKDRVLAAHRYGIKRVILPERNLKDLSEVPLPILSD
MEILLVRRIEEVLDHAFEGRCPLRSRSKL*
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/db_xref="PID:9994897"
/translation="MEHQLLCCEVETIRRAYPDTNLLNDRVLRAMLKTEETCAPSVSY
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GRACHWYDSKKETIPLTAEKLLYTYNBIRPEBLLQWELLIJNBLIKBHPDF
IEHELSKMPRADENKOTIRKHAQTFVALCATDVKFISNPPSWYAAGSVVAAGGLULG
SPNNFLSCYRTTHFLSRVIKCDPDCLRACQEQIEALLESSLRQAQONVDPKATEEEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GenBank staff at the National Library of Medicine created this entry [NCBI gibbs 167715] from the original journal article. This sequence comes from Fig. 1.
Map location: 7.
Location/Qualifiers
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Cyl-1-cyclin Dl [mice, BALB/c, brain, mRNA, 3737 nt].
9994896 '
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Pred. No. 1.76e+00;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
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/note="This sequence comes from Fig. 1."
/codon_start=1
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Pred. No. 1.76e+00;
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/organism="Mus sp."
/db_xref="taxon:10095"
138. .1025
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/gene="Cyl-1"
138. 1025.
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Local Similarity 96.8%;
nes 30; Conservative
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Best Local Similarity 87.2%;
Matches 34; Conservative
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                                                                                     /product="inter-alpha-inhibitor heavy-chain H2"
//bcoduct="inter-alpha-inhibitor heavy-chain H2"
//db_xref="PlD: 3307038"
//db_xref="PlD: 34915954"
//translation="MKGITCFLICFLISEAGCFEIPTNGLSEFAEYGDLAELALGKFH
//translation="MKGITCFLICFLISEAGCFEIPTNGLSEFAEYGDLAELALGKFH
//VPGNRRSQEGVDQYTLYSYKVQSTITSRMANTVIQTKVVNHSPEPQDVYPDIQIPKG
AFISNERSTVORFFYCRALLYMQARKGATRAGLWSRALDMENFRTEVNI
APGARVOFELHYOEVKWHNGSYEHRIHLOPGRLAKHLEVDVOIIEPGGLRFLHYLDT
FDGHFDGVPVVVKGQOKAHVAFKPTVAQQRKCPSCSETAVDGELVVWTDVNREGKAGE
LQLENGYFVHFFAESHDPIPKNILEVTUSOSGWMGITKMGYVFAENTLILDIARDD
FSUVDFNHANTRTWHNDLYSATKTQVADAKTYIEKIQPSGGTNINBEALLAAIFILNBAN
NLGLLDPNSVSLIILVSDGDPTVGELOLSKIOKNVKONIQDNVSLFSLGIGFDVDYDF
LKRLSNDRGWAGNSTYGONDTASOLKKFYNVOSTFLLARNVGFNYPAGSYTDVQNSFP
NFGGSEIVVAGKFNPEKLEOLOGIITAATSAAVELVLETLAEMGSTEAFLAKDBHADP
DFTKKLWAYLTINQLLDERSRAPSAAVKKITKSILQMSLDHHIYTPLTAMVVENEAG
DENMLADAPPQDGSCSGTLAKTGRKYTPNSLPSWYNSDFLAKNSDFLAKDR
DGKLSTYFGKIGFYROPHSASAVENTFNSLPSWYNSDFLAKNVENTFN
DGKLSTYFGKIGFYROHESTETISLSRGSRVSVLLARWSDSALVLANGRVHLSV
KEKTYTTLOGESTEVENTERFINDENTFORMSDELSTR
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/db_xref="PID:g1816586"
/translation="MSDSPVELPSRLAVLPFRNKVLLPGAIVRIRCTNPSSVKLVEQE
LWQNEEKGLIGVLPVRDSEATAVGSLLSPGVGSDSGEGGSKVGGSAVESSKQDTKNGK
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Barakat, S., Pearce, D. A., Sherman, F. and Rapp, W. D.
Barakat, S., Pearce, D. A., Sherman, F. and Rapp, W. D.
Barate contrains a Lon protease gene that can partially complement a yeast piml-deletion mutant
Plant Mol. Biol. 37 (1), 141-154 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Charophyta/Embryophyta group;
Embryophyta; Tracheophyta; seed plants; Magnoliophyta; Liliopsida;
Poales; Poaceae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (14-JAN-1997) Biology, University of Missouri-St. Louis, 8001 Natural Bridge Road, St. Louis, MO 63121, USA
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Zea mays LON1 protease (LON1) mRNA, complete cds.
U85494
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/codon_start=1
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/tissue_type="liver"
/dev_stage="adult"
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/organism="Zea mays"
/strain="B73"
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2 (bases 1 to 3217)
Rapp,W.D. and Barakat,S.
Direct Submission
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Best Local Similarity 78.4%;
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US-08-799-910-9.rge

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AKLLPGRTDNAVKNHWNSTIKRKVETGGFLTVKASGQOEBREDSGYQAAEDQNHVLLS
EPVERGANIPEPSNILSPRLLTKSPGIRSEQDSGGEGSNSSSATAYUDSAPEKWNVE
YNELVPGSDIMESDPEAMCELSSFDLGEDSTVSDVGSPTHAAVTDKPQASNVTEYRL
DGHTLSDLCKGNKGELIPISPOPOTAFGTPPSVLKGNKKRKTILSPYTENGGSITTSY
TEANSMTPKSTPVKSLPFSPSOFLNFWSKQDALELENPSLTSTPVCSOKTMYTPLHR
DKTPLLQKNSYFITPNNKFAADHYLHTPTPFKNALEKFGSLKPLPFTPLLEDLKEVL
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LVKKHGGGEWKTIASNLNNRTEQQCQHRWLRVLHPDLVKGPWTKEEDEKVIELVKKYG
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TQCSLRNTETATPFKTENGTFTNTDLCPQSLMDLDTFHSTAVGSNKCPTIKTETLFQV
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                                                                                                                                                                                                                      Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea;
Pipidae; Kenopodinae; Kenopus.
1 (bases 1 of 3789)
Bouwmeester, T., Guehman, S., El-Baradi, T., Kalkbrenner, F., Van
                                                                                                                                                                                                                                                               Journmeester, T., Guehmann, S., El-Baradi, T., Kalkbrenner, F., Van Wijk, D., Moelling, K. and Pieler, T.
Molecular cloning, expression and in vitro functional
characterization of Myb-related proteins in Xenopus
Mech. Dev. 37, 57-68 (1992)
                                                                                               11-SEP-1992
complete cds
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Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 4624)
Hao.L., Baskerville,C. and Charbonneau,H.
Direct Submission
Submitted (08-MAY-1998) Biochemistry, Purdue University, 1153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KPEKTKMORHNIMNIPEPMTAAWKTVAFGGSQDQMMLFLSCTVALLILRFS"
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Homo sapiens Cdc14B1 phosphatase mRNA, complete cds.
AF064104
93136331
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                                                                                   XELMYBRP1 3789 bp mRNA VRT
Xenopus laevis myb-related protein 1 (myb1) mRNA,
M75870
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Pred. No. 6.55e-01;
0; Mismatches 11; Indels
                                                                                                                                                                   myb-related protein 1.
Xenopus laevis gastrula, oocyte cDNA to mRNA.
/product-"myb-related protein 1"
                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
1. .3789
/organism="Xenopus laevis"
/db_xref="taxon:8355"
/dev_stage="gastrula, oocyte"
61. .2262
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61. .226?
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Matches 47; Conservative
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similar to the product encoded by GenBank Accession Number AF023158; putative alternatively spliced variant encoded by GenBank Accession Number AF064105"
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/db_xref="PlD:g3136332"
/db_xref="PlD:g3136332"
/db_xref="PlD:g3136332"
/db_xref="PrD:g0136332"
/db_xref="PrD:g0136333"
/db_xref="MKRKSERSSAWHYF51DNELEYENFYADFGPLNLAMYRYCC RINKKLKSITMLRKKIVHFTGSDQNRVQANAAFLVGCYMVIYLGRTPEEAYRILIFGET
                                                                                                                                                                                                                                                                                                                                                           /note="CDC14B; similar to Saccharomyces cerevisiae Cdc14p;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AF090113 5433 bp mRNA ROD 20-SEP-1998
Rattus norvegicus AMPA receptor binding protein mRNA, complete cds.
AF090113
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/Laxsef-pitD:g3638077"
/translation-"YMPLIKERSSTLGLTISGGTDKDGKPRVSNLRPGGLAARSDLLN
VGDYIRSVNGIRLTRLRHDEIITLLKNVGERVVLEVEYELPPPAPENNPRIISKTVDV
STXEKONSFRYLRGGAHEDLHKSRPLVLTYVRPGGPADRESSEKVORPLLSIDGIPL
HGASHATALAGGSTBALEOVEDVAATADGAGPLVVEIAKTPGSALGISLTI
GSHRNKPAITIDRIKPASVVDNSGALHAGDHILAIDGTSTEHCSLVEATKLLASVTEK
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Structure, Industrial Control Cont
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Submitted (03-SEP-1998) Howard Hughes Medical Institute and Dept.
of Biochemistry, New York University, 550, First Avenue, New York,
NY 10016, USA
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Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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Srivastava,S., Villm,F.S., Khatri,L., Daly,C. and 2iff,E.B.
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1. .4624
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Pred. No. 1.76e+00;
0; Mismatches 6
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/db_xref="taxon:10116"
295. .2763
                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/tissue_type="placenta"
453. .1949
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Best Local Similarity 85.4%;
Matches 35; Conservative
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Homo sapiens
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*** SEQUENCING IN PROGRESS *** Plasmodium falciparum 3D7 chromosome
12 PFYAC812 genomic sequence; HTGS phase 1, 31 unordered pieces.
OSRSYSSTPFSSPTMNPAFPCANASTLPRGPMSPRTTAGRRRORRKEHRSSLSLASST
VGPGGOLVHTETTEVVLGOPLSGFGLQGGGTFATFTLSSPPLWFFTEPDSPAERCG
LLQVGDRVLAINGIATEDGBABANQLLRDAALARWYLEIEFDVAESVIPSGFTEPDSPAERCG
LLQVGDRVLAINGIATEDGBARQLLISDIKKGSVAHRYTELEFDVAESVIPSGFTFH
CPMEYAVQILRQCEDLVKLKIRKDEDNSDEQESSGAVSTYELKRYGGPLGITISGTE
KIKKQLDRPLLPRQSGSLSEAGAIVGBRLAINSVSLKGRPLESFAILLLQVAGETYTL
KIKKQLDRPLLPRQSGSLSEAGAIVDSPPEAALKGGLLTTHFSPAVPSVDSAVESVSTAS
ATEGGFGGSGSSTPPQVAVRSYTPQGMRSSRLKSSPPPLEPRRTSYTFGPTDESFPEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             * This sequence is unfinished. It consists of 31 contigs for * which the order is not known: their order in this record is * arbitrary. In some cases, the exact lengths of the gaps * between the contigs are also unknown; these gaps are presented * as runs of N as a convenience only. When sequencing is complete, the sequence data presented in this record will be replaced * by a single finished sequence with the same accession number.
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Hyman, R.W., Qin, F., Fung, E.L., Conway, A.B. and Davis, R.W.
Direct Submission
Submitted (18-FEB-1998) Stanford DNA Sequencing and Technology
Center, Stanford University, 855 California Avenue, Palo Alto, 94304, USA
                                                                                                                                                                                                                   Gaps
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HTGS. HTGS_PHASE1.
HTGS. HTGS_PHASE1.
Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 224645)
Hyman, R. W., Qin, F., Fung, E.L., Conway, A. B. and Davis, R. W.
Plasmodium falciparum 3D7 chromosome 12
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of 7660 bp in length
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Pred. No. 1.76e+00;
0; Mismatches 5;
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Matches 34; Conser
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KEYWORDS
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RESULT

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ORIGIN

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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.

I bases 1 to 232)

Myers, R.M.

Unpublished (1995)
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1. .224645
/organism="Plasmodium falciparum"
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Pred. No. 1.76e+00;
0; Mismatches 8
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a 24151 c 23142 g 89614
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human STS SHGC-15668.
G15123
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                                                145281:
                                                                    153810:
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                                                                                                                                                  179241:
         127925:
                            136715:
                                                                                         160405:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 2.4%;
Best Local Similarity 82.2%;
Matches 37; Conservative
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/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
                                                                                                                                                                 Protocol
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primer_bind
BASE COUNT
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             G37172 350 bp DNA STS 30-MAR-1998
SHGC-57073 Human Homo sapiens STS genomic, sequence tagged site.
G37172
92996823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 350)
Myers,R.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Prepared with primer pairs derived from R05470 -- Merck/UniEST
                                                                                                                                                                                                    degrees C for 15 seconds degrees C for 23 seconds degrees C for 30 seconds
                                                                                                                                                                         Initial incubation: 94 degrees C for 90 seconds
             Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, M-344, Stanford, CA 94305, USA
Tel: 4157259687
Fax: 4157259689
Email: myers@shgc.stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Richard M. Myers
Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, M-344, Stanford, CA 94305, USA
Tel: 4157259687
Fax: 4157259689
Email: myers@shgc.stanford.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8; Indels
                                                                                                                                                                                                    94 degrees C for 15
62 degrees C for 23
72 degrees C for 30
30
Perkin Elmer 9600
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Pred. No. 4.65e+00;
                                                                                                                                                                                                                                                                                          25 ng
each 1 uM
each 200 uM
0.05 units/ul
10 ul
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                                                                                                               Primer A: ACTITITCTCCTTCAAGAGTCACC
Primer B: TGCACTTTCATTCACATGCA
STS size: 132
PCR Profile:
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83. 214
83. .106
complement(195. .214)
a 45 c 31 g 79
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50
20
8.3
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Contact: Richard M. Myers
                                                                                                                                                                                                                     Annealing:
Polymerization:
PCR Cycles:
Thermal Cycler:
                                                                                                                                                                                                                                                                                                                    dNTPs:
Taq Polymerase: (
Total Vol:
                                                                                                                                                                                                    Denaturation:
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2.3%;
Best Local Similarity 81.0%;
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                               KCl:
Tris-HCl:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human STSs (1997)
Unpublished (1997)
                                                                                                                                                                                                                                                                                          emplate:
                                                                                                                                                                                                                                                                                                         Primer:
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primer_bind
BASE COUNT
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DEFINITION
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AUTHORS
TITLE
JOURNAL
COMMENT
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NID
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g

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ocu41441 571 bp DNA INV 02-MAR-1996
Dosophila melanogaster macrolide binding protein (FKBP12) gene,
U41441
g1209721
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Drosophila melanogaster

Drusophila melanogaster

Drusophila melanogaster

Brusryctes, mitcochondrial eukaryotes; Metazoa; Arthropoda;

Trachasta; Insecta; Pterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidee; Drosophila.

1 (bases 1 to 571)

Wang,T., Li,B.Y., Danielson,P.D., Shah,P.C., Rockwell,S.,

Lechleider,R.J., Martin,J., Manganaro,T. and Donahoe,P.K.

The Immunophilin FKBP12 Functions as a Common Inhibitor of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tur Full for the description of the following the following the following for the fo
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1. 350
//Organism="Homo sapiens"
//db_xref="taxon:9606"
                                                                                                                                                                                                                                      94 degrees C for 30 seconds 60 degrees C for 30 seconds 72 degrees C for 23 seconds 30 Perkin Elmer 9700
                                                                                                                                                          Initial incubation: 95 degrees C for 10 minutes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          each 1 uM
each 200 uM
0.07 units/ul
5 ul
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Total Vol:
Primer A: CAACITIGCAAAATCCIGGAAG
Primer B: TACCAGGGTGGCCAGAAAG
STS size: 114
PCR Profile:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /ding___/close_lib="Human"
234. .347
234. .255 complement(328. .347)
a 56 c 57 g 1
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50 mM
10 mM
8.3
                                                                                                                                                                                                                                          Denaturation:
Annealing:
Polymerization:
PCR Cycles:
                                                                                                                                                                                                                                                                                                                                                                                                         Thermal Cycler:
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pH:
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Gaps

ö

gene

CDS

173

BASE COUNT

ORIGIN

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/db_xref="PID: 9249371"
//db_xref="PID: 9249371"
//translation="EDPGVAMGRRPARCYRYCKNKPYPKSRFCRGVPDAKIRIFDLGR
KRAKVDEFPLGGHMYSDEYEQLSSEALEAARICANKYMVKSGGKDGFHIRVRLHPFHV
KRAKVDEFPLGGHMYSDEYEQLSSEALEAARICANKYMVKSGGKDGFHIRVRLHPFHV
INTRINKHLSCAGDBLQHRGFFTLAKLSCPSAPSGRTRSM"
197 c 194 g 165 t
                                                                                                                                                                                                                                                                                                                                                                              S35960 739 bp mRNA PRI 04-SEP-1992 laminin receptor homolog [3' region] [human, mRNA Partial, 739 nt]. S35960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GenBank staff at the National Library of Medicine created this entry [NCBI glubbs 103309] from the original journal article. This sequence comes from Fig 2a. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence comes from Fig 2a."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA cloning and genomic analysis of a new multigene family scommon phylogenetic and expression profiles with the laminin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryotae: mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 739)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bignon, C., Roux-Dosseto, M., Zeigler, M.E., Wicha, M.S. and Martin, P.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biochem. Biophys. Res. Commun. 184 (3), 1165-1172 (1992)
92272704
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                                                                                                                                                       Length 648;
                                                                                                                                                     Score 28; DB 26; Length 648
Pred. No. 4.65e+00;
0; Mismatches 5; Indels
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Soares_placenta_lNHP"
/clone="IMAGE:137079"
101 c 110 g 204 t
                                                                                                                                                                                                                                                                     1222 TITITITITITITITITIGACAGTAAATCAATITIAIT 1185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="clone 48-1"
/gene="laminin receptor homolog"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              homolog"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 28; DB 25;
Pred. No. 4.65e+00;
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Homo sapiens clone 24651 mRNA sequence.
AF070648
93283922
FLI_CDNA.
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                                                                                                                                                                                                                                              1. .739
/organism="Homo sapiens"
/db_xref="taxon:9606"
2. .463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="laminin receptor/note="C-terminal. This
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Best Local Similarity 83.3%;
Matches 35; Conservative
                                                                                                                                                       2.3%;
Similarity 86.8%;
33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /partial
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University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
SUBMITTED BY:
                                                                                                                                                                            /product-"macrolide binding protein"
/bc.xref-"PID:91209722"
/tab.slation-"MGVQVVPIAPGGGSTYPRNGGKYTVHYTGTLDDGTKFDSSRDRN
KPFKFTIGKGEVIRGMDGVAQLSVGGSAKLICSPDYAXGSRGHPGVIPPNSTLFEDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            attempt has been made to verify whether this corresponds to the full-length of the original mRNA from which it was derived. We have tried to obtain doubbe-stranded, or double chemistry sequence across the entire clone, but potentially, there are areas in the sequence where this level of coverage was not achieved.

Nevertheless, we are confident of the accuracy of this sequence as all regions of low quality, as defined by PHRAP (P. Green, in preparation), were visually inspected and edited accordingly The consensus quality values for this sequence have been submitted separately.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Woessner, J., Tan, F., Marra, M., Kucaba, T., Yandell, M., Martin, J., Marth, G., Bowles, L., Wylie, T., Bowers, Y., Steptoe, M., Theising, B., Geisel, S., Allen, M., Underwood, K., Chappell, J., Person, B., Gibbons, M., Marvey, N., Pape, D., Chamberlain, A., Morales, R., Schurk, R., Ritter, E., Kohn, S., Swaller, T., Behymer, K., Hillier, L., Wilson, R. and Waterston, R.
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Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 4.65e+00;
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Homo sapiens full length insert cDNA YH91B08
AF07493
3737531
FLI_CDNA.
                     /note="FK506-binding protein 2"
/gene="FK506-bp2"
/allele=""
                                                                                        /db_xref-"FlyBase:FBgn0013954"
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Department of Genetics
Washington University
St. Louis MO 63108, USA
http://genome.wustl.edu/gsc
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                                                                                                                                                                                                                                                                                            132
                                                                                                                                     /gene-"FK506-bp2"
                                                                                                                                                            /codon_start=1
                                                                                                                                                                                                                                                                                                                                                           Ouery Match 2.3%;
Best Local Similarity 75.9%;
atches 41; Conservative
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02-JUL-1998

source

FEATURES

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WERFWHSRDHLVSTSALDFLDKLLRYDHQARLTARGAMDHPYFYPIVKDGRGAPAA
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DSCHFNKGTVGATDRGFTDIPQGDEKKMAEAVATVGPVSVAIDASHESFQFYSEGVYN
EPQCDAQNLDHGVLVVGFGTDESGEDYMLVKNSWGTTWGDKGFIKMLRNKENQCGIAS
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Drosophila melanogaster cysteine proteinase 1 (CP1) mRNA, complete
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Trysellus,Y. and Hultmark,D.
Cysteine proteinase 1 (CPI), a cathepsin L-like enzyme expressed the Drosophila melanogaster hemocyte cell line mbn-2
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Tracheata; Hexapoda; Insecta; Pterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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    1435
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Pred. No. 4.65e+00;
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Pred. No. 4.65e+00;
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/note="cathepsin L homolog"
                                                                                                                                                                                                            372
                                                                                                                                                                                                          311 g
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Trysellus, Y. and Hultmark, D.
Direct Submission
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/gene="CP1"
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Best Local Similarity 86.8%;
Matches 33; Conservative
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Best Local Similarity 81.8%;
Matches 36; Conservative
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Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1332)
Andersson, B., Wentland, M.A., Ricafrente, J.Y., Liu, W. and Gibbs, R.A. A'double adaptor' method for improved shotgun library construction 96207227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      l (bases 1 to 1404)
Daniotti,J.L., Allende,M.L., Weinberg,E.S. and Allende,J.E.
Cloning and expression of genes coding for protein kinase CK2 alpha
and beta subunits in zebrafish (Danio rerio)
CEll. Mol. Biol. Res. 40 (5-6), 431-439 (1994)
                                                                                                                                                                                                                                                                                                                                              Human Genetics, Baylor
S930, Houston, TX 77030, USA
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Vertebrata; Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Ostariophysi; Cypriniformes; Cyprinoidea; Cyprinidae; Rasborinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GenBank staff at the National Library of Medicine created this entry [NCBI glabsq 163821] from the original journal article. This sequence comes from Fig. 1A.

Location/Qualifiers
                                                                                                                                                                                 Yu,W., Andersson,B., Worley,K.C., Muzny,D.M., Ding,Y., Liu,W., Ricafrente,J.Y., Wentland,M.A., Lennon,G. and Gibbs,R.A. Large-scale concatenation CDNa sequencing Genome Res. 7 (4), 353-358 (1997)
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/note="protein kinase; This sequence comes from Fig.
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casein kinase 2 alpha subunit-protein kinase [Danio
rerio-zebrafish|embryos, mRNA Partial, 1404 nt].
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Pred. No. 4.65e+00;
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Submitted (05-JUN-1998) Molecular and
College of Medicine, One Baylor Plaza
Location/Qualifiers
1..1332
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/clone=lib="lnis"
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/organism="Danio rerio"
/db_xref="taxon:7955"
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                                                                                                                                                              (bases 1 to 1332)
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Yu, W. and Gibbs, R.A.
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Matches 33; Conservative
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/product-"SEB4"

About to 14407468"

/translation-"HILOPACSPSVEPRPSAAPSAMHGSRKDTTFTKIFVGGLPYHTT
DASLRKYFEGFGDIEEAVVIIDRQTGKSRGYGFVTMADRAAADRACKDPNPIIDGRKA
                                                                                                                                                                                                                                                                                                                                                                                NMESLPTVHNEGPSSAEGKDIAFSPPVYPAGILLVCNNCAAYRKLLEAOTPSVRKWAL
RRONEPLEVELCRLERERTAKKSREDNETPEEREVRRHEDREAKRLORMGETDEGRAR
RLORDREAMRLKRANETPEKROARLIREREAKRLKRRLEKMDWALRAQFGGDPSAMAA
LAAENNFFCLPVSGYELDSQLLGKMAFEEGNSSSLH"
4 480 c 537 g 369 t
                                                                                                                                                                                                                                                                                         /product-"unknown"
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/tzanslation-"MSRRKOTNPNKYHCDSEGDEETTODEVSSHTSEEDGGVVKVEK
ELENTEOPVGGNEVVEHEVTGNLNSDPLLELCQCPLCQLDCGSREQLIAHVYQHTAAV
                                                                                                                                                                                                                                                                                                                                                                 VSAKSYMCPVCGRALSSPGSLGRHLLIHSEDQRSNCAVCGARFTSHATFNSEKLPEVL
3 (bases 1 to 1841)
Yu,W. and Gibbs,R.A.
Direct Submission
Submitted (05-740-1998) Molecular and Human Genetics, Baylor
College of Medicine, One Baylor Plaza S930, Houston, TX 77030, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (30-SEP-1993) A. Ruehlmann Cec, Medizinische Hochschule
Hannover (MHH), Institut fuer Molekularbiologie, OE5250, I4 Raum
2630, 30633 Hannover, FRG
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
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                                                                                                                                                                              /dev_stage="infant"
/tissue_type="brain"
/clone="I.M.A.G.E. Consortium clone ID 24554"
377. .1489
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A novel murine RRM-type protein and its human homolog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1841;
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Pred. No. 4.65e+00;
0; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seb4D gene; SEB4D protein; ssDNA binding protein. house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus-musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="lambda gt22 (clontech)"
236. .1863
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                                                                                                           1. .1841
/organism="Homo sapiens"
/db_xref="taxon:9606"
/sex="female"
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236. .940
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X75316
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Ruehlmann, A.C.E.C.
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Best Local Similarity 79.2%;
Matches 38; Conservative
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96207227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (22-NOV-1996) Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza S930, Houston, TX 77030, USA similar to human oligodendrocyte myelin glycoprotein gene sequence with GenBank Accession Number L05367.

Location/Qualifiers
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/clone_lib="Soares library lNIB from IMAGE consortium"
1 278 c 274 g 549 t
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Yu,W., Andersson,B., Worley,K.C., Muzny,D.M., Ding,Y., Liu,W.,
Ricafrente,J.Y., Wentland,M.A., Lennon,G. and Glbbs,R.A.
Large-scale concatenation cDNA sequencing
Genome Res. 7 (4), 353-358 (1997)
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Yu,W., Andersson,B., Worley,K.C., Muzny,D.M., Ding,Y., Liu,W.
Lafafrente,J.Y., Wentland,M.A., Lennon,G. and Gibbs,R.A.
Large Scale Concatenation cDNA Sequencing
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Primates; Catarrhini: Hominidae; Homo.
1 (bases 1 to 1841)
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Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1659)
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Best Local Similarity 82.4%; Pred. No. 4.65e+00;
Matches 42; Conservative 0; Mismatches 8;
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                                                                           HSU/9276 1659 bp mRNA
Human clone 23960 mRNA sequence.
U79276
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NVNLAYLGAKPRSLOIGFAVGVQQLHPTLIORTYGLTPHYIYPPAIVOPSVVIPATPV PSLSSPYLEYTPASPAXQYPPAIYDQYPYAASPAAGISFVGYGYPAAVPQALSAAAP AGTIFVOYQAPQLQPDRMQ" 335. .353 //gene"seb4"
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/db_xref="PID:953814"
/db_xref="SWISS-PROT | 19221"
/translation="WSHYRGLGLPGCALAALVSLVHSQHVFLAPQQALSLLQRVRRA NSGFLEELRKGNLERECVEEQCSYEEAFEALESPQDTDVFWAKYTVCDSVRKPREFFM
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TTNINEIQPSVLQVVNLPIVERPVCKASTRIRITDNMFCAGFKVNDTKRGDACEGDSG
GPFVMKSPFNNRWYQMGIVSWGEGCDRKGKYGFYTHVFRLKRWIQKVIDQFG"
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LRPLFEKKSLKDTTEKELLDSYIDGRIVEGWDAEKGIAPWQVMLFRKSPQELLCGASL
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (17-APR-1940) Friezner Degen S.J., Childrens Hospital Research Foundation, IDR Room 601, Elland Bethesda Ave., Cincinnati, Ohio 45229, USA (bases 1 to 2031)
Degen.S.J., Schaefer.L.A., Jamison,C.S., Grant,S.G., Fitzgibbon,J.J., Pai,J.A., Chapman,V.M. and Elliott,R.W. Characterization of the cDNA coding for mouse prothrombin and localization of the gene on mouse chromosome 2
DNA Cell Biol. 9 (7), 487-498 (1990)
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                                                                                                                                                                                                                                                                                                                                     Gaps
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1. .2031
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Pred. No. 4.65e+00;
0; Mismatches 12; Indels
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/note="signal peptide (AA -43 to -1)"
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/strain="C57BL/6"
/db_xref="taxon:10090"
/tissue_type="liver"
/cione_lib="Lambda gt10"
19. 1875
                                                                                                                                                                                                                                    523 g
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Mouse mRNA for prothrombin.
X52308
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Best Local Similarity 78.0%;
Matches 46; Conservative
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1 (bases 1 to 2031)
Friezner degen, S.J.
Direct Submission
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Gaps
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                                                                                              Length 2031;
                                                                                              Score 28; DB 28; Length 203
Pred. No. 4.65e+00;
0; Mismatches 5; Indels
148. .1872
/note="mature protein (AA 1-575)"
1988
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                                      /note="polyA tail"
519 c 569 g
                                                                                                Query Match 2.3%;
Best Local Similarity 86.8%;
Matches 33; Conservative
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 mat_peptide
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PROKARYOTA: GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
ENTEROBACTERIACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 H-A-P-P.
H-A-P-P.
2 X 7 AA TANDEM REPEATS OF T-H-R-H-A-P-P.
                                                                                                                                                                                         BOYD A.C., ARCHER J.A.K., SHERRAIT D.J.;
MOL. GEN. GENET. 217.488-498 (1989).
-1- FUNCTION: THIS PROTEIN IS ESSENTIAL TO PROMOTE THE SPECIFIC
TRANSFER OF THE PLASMID IN THE PRESENCE OF CONJUGATIVE PLASMIDS.
-1- SIMILARIY: HIGH, TO THE MBAA AND MBKA PROTEINS OF E.COLI.
PIR; JQ0390; JQ0390.
                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KELLER B., LAMB C.J.;
GENES DEV. 3:1639-1646(1989).
-!- FUNCTION: HAS A SPECIALIZED STRUCTURAL FUNCTION, POSSIBLY IN
THE MECHANICAL PENETRATION OF THE CORTEX AND EPIDERMIS OF THE
                                                                                                                                                                                                                                                                                                                                                                                                 431 GERLRGIAEDVFAYAT-GORDAERAGHAVESAGAALERADRTLEP-VIORELEIRE 484
                                                                                                                                                                                                                                                                                                                                                                                                                    26 GPR-RGSGPEIFTFDPLPEPAAAPAGRPSASRGHR-KRSRRVLYPRVVRRQLDVEE 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JAN-1990 (REL. 13, CREATED)
01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)
01-MAR-1992 (REL. 21, LAST ANNOTATION UPDATE)
EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).
                                                                                                                                                                                                                                                                                                                                                                        ٠.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NICOTIANA TABACUM (COMMON TOBACCO).
EUKARYOTA: PLANTA: EMBRYOPHYTA: ANGIOSPERMAE; DICOTYLEDONEAE;
SOLANALES; SOLANACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X13885; G19867; -
PIR; S06733, 806733.
HSSP, P19999; LGL
REPEAT; CELL WALL; GLYCOPROTEIN; SIGNAL; STRUCTURAL PROTEIN;
                                                                                                                                                                                                                                                                                                                                        8.3%; Score 93; DB 1; Length 517; 32.1%; Pred. No. 2.54e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 620;
                                                                                                                                                                                                                                                                                                                                                                     21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SUBCELLULAR LOCATION: EXTRACELLULAR MATRIX.
-!- PIM: EXTENSINS CONTAIN A CHARACTERISTIC REPEAT OF TH
SER-PRO(4). THE PROLINE RESIDUE IS HYDROXYLATED AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONTAINS THE SER-PRO(4)
3 X APPROXIMATE TANDEM R
EC549236 CRC32;
                                                                                                                                                                                                                                                                                             PLASMID; MOBILITY PROTEIN; CONJUGATION.
SEQUENCE 517 AA; 57808 MW; 445FBC4A CRC32;
               CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                      13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EXTENSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8.3%; Score 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-CV. XANTHI; TISSUE-LEAF;
MEDLINE; 90128263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ₩,;
P13658;
01-JAN-1990 (REL. 13, CREATE
01-JAN-1990 (REL. 13, LAST 5
01-MAY-1992 (REL. 22, LAST F
MOBILIZATION PROTEIN MBEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65406
                                                                                                                                                                                                                                                                                                                                                                      18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70
1229
229
236
205
205
205
AA;
                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE; 89364735.
                                                                                        ESCHERICHIA COLI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLYCOSYLATED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HYDROXYLATION.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LT 40
EXTN_TOBAC
P13983;
                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
REPEAT
DOMAIN
REPEAT
REPEAT
REPEAT
DOMAIN
                                                                           MBEA
                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 94023929.

A BENNETT M., REED R.;
SCIENCE 262:102-108(1993).

- I- FUNCTION: SUBUNIT OF THE STABLE BINDING OF UZ SNRNP TO THE ASSEMBLY FORMED BY THE STABLE BINDING OF UZ SNRNP TO THE BRANCHPOINT SEQUENCE (BPS) IN PRE-MRNA. SEQUENCE INDEPENDENT BRANCHPOINT SEQUENCE (BRS) IN PRE-MRNA. SEGUENCE STABLE BINDING OF SF3A/SF3B COMPLEX USSTREAM OF THE BRANCH SITE IS ESSENTIAL, IT MAY ANCHON TO THE PRE-MRNA.

- I- SIBUNIT: SF3A IS COMPOSED OF SAPS 61, 62 AND 114 (SF3A60, SF3A66 AND SF3ALOR ESPECTIVELY).

- I- SUBUNIT: TO YEAST PRP11.

- SIMILARITY: TO YEAST PRP11.

- SIMILARITY: TO YEAST PRP11.
                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  381 РААРАVHPQAPGVHPPAPGMHPQAPGVHPQPPGVHPSAPGVHPQPPGVHPSNPGVHPPTP 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      - YPRVVRRQLP-VEEPNPAKRLLFLLTIVFCQILMAEEGVPAPLPPEDAPNAASLAPTP 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        323 HPPTSGVHPPAPGVHPPAPGVHP-PAPGVHPPAPGVHPPA-PGVHPPPSAGVHPQAPGVH 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 HPIMIILQAPIPA-PSIIPGPRRGSGPEIFIFDPLPEPAAAPAGRPSASRGHRKRSRRVL 66
                                                                                                                                                                                       19 TSHGNATI-ETPSPAAAISVANRIRNAGPRLLFLMNIAAESSAKPVWGPPNFCAAAARMQ 77
                                                                                                                                                                                                        Gaps
                                             WALSH S.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                               EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 93; DB 1; Length 464; Pred. No. 2.54e+00;
                                                                                                                               / Match 8.3%; Score 93; DB 1; Length 350; Local Similarity 30.4%; Pred. No. 2.54e+00; nes 24; Conservative 22; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38; Mismatches 57; Indels
                                         OLIVER K., HARRIS D., BARRELL B.G., RAJANDREAM M.A., SUBMITTED (JUL-1996) TO EMBL/GENBANK/DDBJ DATA BANKS. EMBL. 271137, E254685; --
HYPOTHETICAL PROTEIN.
SEQUENCE 350 AA; 37024 MW; 78B09BFD CRC32;
                                                                                                                                                                                                                                                                                                                                                                01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SF3A66).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WRNA PROCESSING; MRNA SPLICING; NUCLEAR PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POLY-PRO.
E3C651FF CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 517 AA.
                                                                                                                                                                                                                                                                                                                                         464 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POLY-PRO.
POLY-PRO.
                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49196 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 25.5%;
Matches 35; Conservative
                                                                                                                                                                                                                                                                   SRRVL-YPRVVRR-QLPVE 78
                                                                                                                                                                                                                                                   DVRVLMHPKTGRAFRSPVE 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ::|:| | | || |::
125 VSPVLEPFNLTSE-PSD 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            441 MPPMLRP-PLPSEGPGN 456
                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         236
256
                                                                                                                                                                                                                                                                                                                                                                                                                                            HOMO SAPIENS (HUMAN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  464 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE; 94023929.
               SEQUENCE FROM N.A.
                              STRAIN-H37RV;
OLIVER K., HA
                                                                                                                                                                                                                                                                                                                       /LT 38
SP62_HUMAN
Q15428;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LT 39
MBEA_ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
SEQUENCE
                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                 78
                                                                                                                                                                                                                                                                            62
                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
ID MB
                                                                                                                                                                                                                                           q
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MISSING (IN VARIANT 6).
MISSING (IN VARIANT 3).
MISSING (IN VARIANT 3).
MIGUPSPRATDPPSHLDGPPA -> GESLTCFQPRGHWVE
MGGMIGY (IN VARIANTS 2, 5, AND 6).
MISSING (IN VARIANTS 3 AND 4).
                                                                                                        MISSING (IN VARIANTS 3 AND 4).
LDGPPAVAVGQCPLVGPGPMHRRHLLLPARIPRGLSEARC
                                                                                                                                   LLLFAAALAAAATLGCTGLVAYTGGLTPVWCFPGATFAP
-> MAPRPWLMASARWWGQAPCTAVTCCSLPGSLGLAYPRR
VACSCSPLLWLLPPHWAALGWWPIPAVSPQSGVSREPPSPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75 ORTVTVEDLEPGKKYKFLLYGLLGGKRLGPVSALGMTAPEEDTP-APELAPEAPEPPEEP 133
                                                                                                                                                                                                                                                                       518 HVRQLQERMEMLQAPGAAAITGVPSPR-ATDPPSH-LDG-P-PAVAVGQCPLVGPGPMHR 573
                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENE LOCUS.
-!- SIMITARITY: CONTAINS A DOMAIN RELATED TO THE C-TERMINAL PART THE BETA AND GAMMA CHAINS OF FIBRINOGEN.
-!- SIMILARITY: CONTAINS 6 FIBRONECTIN TYPE III-LIKE DOMAINS.
EMBL; M25813; G183070; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOREL Y., BRISTOW J., GITELMAN S.E., MILLER W.L.;
PROC. NATL. ACAD. SCI. U.S.A. 86:5582-6586(1989).
-!- FUNCTION: NOT NOWN. THIS PROTEIN IS ENCODED ON THE OPPOSITE
STRAND OF THE STEROID 21-HYDROXYLASE/COMPLEMENT COMPONENT C4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     - : = : : : : -
                                                                                                                                                                                                                  DB 1; Length 631;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 820;
                                                                                                                                                                          EP (IN VARIANTS 3 AND 4).
C5E410E8 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
FIBRINOGEN BETA/GAMMA.
BY SIMILARITY.
  (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 92; DB 1; I
Pred. No. 3.34e+00;
14; Mismatches 25
                                                                                                                                                                                                                              Pred. No. 3.34e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EF594B45 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                  01-AUG-1991 (REL. 19, CREATED)
01-AUG-1991 (REL. 19, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
FIBRINOGEN-LIKE PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                            15; Mismatches
              SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
                                                                                                                                                                                                                  Score 92;
                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89601 MW;
                                                                                                                                                                                        69601 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8.3%; s.larity 33.3%; E.Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : = ::: := : ::
                                                                                                                                                                                                                Watch 8.3%;
Local Similarity 35.5%;
hes 27; Conservative
                                                                                                                                                                                                                                                                                                                           574 -RHLLLPARIPRPGLS 588
                                                                                                                                                                                                                                                                                                                                           |::| | |: | |:
62 SRRVLYP-RVVRRQLP 76
                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
  100
195
604
356
382
448
                                                                                                         631
631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22
126
226
328
328
509
509
606
758
758
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 20; Conser
                                                                                                                                                                                          631 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 89367293.
  100
195
328
378
412
536
                                                                                                                                                                                                                                                                                                                                                                                                         FIBL_HUMAN P22105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
BINDING
ACT_SITE
DOMAIN
                                      VARSPLIC
VARSPLIC
VARSPLIC
VARSPLIC
                                                                                                        VARSPLIC
VARSPLIC
                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOMAIN
                                                                                                                                                                                                                                            Matches
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  a
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                                                                                                                                                                                                                                                                                                                                                      ò
              'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUES CONTAINING SMOOTH MUSCLE.
ALTERNATIVE PRODUCTS: FIVE ISOFORMS DIFFERING IN THE C-TERMINAL
ARE PRODUCED AS A RESULT OF ALTERNATIVE SPLICING. THE LONGEST ONE
                                        173 SRHGHPPPPTYAQPPPTPIXSPSPQVQPPP---TYSP-PPPTHVQPTPSPPSRGHQPQPP 228
                                                        01-0CT-1996 (REL. 34, CREATED)
01-0CT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
MYOTONIN-PROFIED KINASE (EC 2.7.1.-) (MYOTONIC DISTROPHY PROTEIN
KINASE) (MDPK) (DM-KINASE) (DMK) (DMPK) (MT-PK).
DMPK OR MDPK OR DMIS.
HUS MUSCULUS (MOUSE).
EUKARYOTA: METAZOA: CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             G., WORMSKAMP N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (VARIANT 1) IS SHOWN HERE. SIMILARITY: WITH THE CONSERVED CATALYTIC DOMAINS OF SER/THR-
                                                                                                                                                                                                                                                                                                                                                                  MAHADEVAN M.S., AMEMIYA C., JANSEN G., SABOURIN L., BAIRD S.,
NEVILLE C.E., WORMSKAMP N., SEGERS B., BATZER M., LAMERDIN J.,
DE JONG P., WIERINGA B., KORNELUK R.G.;
HUM. MOL. GENET. 2:299-304(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGD; MGI:94906; DM15.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00108; PROTEIN_KINASE_AT; 1.
PROSITE; PS50011; PROTEIN_KINASE_DM; 1.
TRANSFERASE; SERINE/THREONINE-PROTEIN KINASE; ATP-BINDING;
ALTERNATIVE SPLICING.
PROTEIN KINASE; ATP-BINDING;
PROTEIN KINASE; ATP-BINDING;
NP_BIND 77 85 ATP (BY SIMILARITY).
 Pred. No. 3.34e+00; 20; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 117-631 FROM N.A. (VARIANTS 3; 4; 5 AND 6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JANSEN G., BARTOLOMEI M., KALSCHEUER V., MERKK G
MARIMAN E., SMEETS D., ROPERS H.-H., WIERINGA B.
HUM. MOL. GENET. 2:1221-1227(1993).
                                                                                                                                                                          631 AA
                                                                                                                                                                          PRT;
                                                                                           229 THRHAPPTHRAPPTHQPSPLRHL 252
                                                                                                           : : | : | : | : | 64 RVLYPRVVRRQLP-VEEPNPAKRL 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; 238015; G56526; -
EMBL; 238015; G565903; -
EMBL; 221503; G556903; -
EMBL; 221504; G556903; JOINED.
EMBL; 221506; G556903; JOINED.
EMBL; 201506; G556903; JOINED.
EMBL; S60313; G300257; -
EMBL; S60315; G300255; -
EMBL; S60316; G300255; -
Best Local Similarity 27.4%;
Matches 23; Conservative
                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                             EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-129/SV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 94004865.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 93251003.
                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE; 93271990.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-BRAIN;
                                                                                                                                                             JT 41
DMK_MOUSE
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-1- CATALYTIC ACTIVITY: S-ADENOSYL-L-METHIONINE + RRNA - S-ADENOSYL-L-HOMOCYSTEINE + RRNA CONTAINING N(6)-METHYLADENINE.
-1- SIMILARITY: BELONGS TO THE RRNA ADENINE N-6-METHYLLTRANSFERASE
                                                                                                                                                                                                                  ARTHROBACTER SP. (STRAIN B3381).
PROKARYOTA; FIRMICUTES; IRREGULAR ASPOROGENOUS RODS; CORYNEFORM GROUP.
                                                                                                                                                                                                                                                                                                      STRAIN-H37RV;

GLUVER K. HARRIS D., BARRELL B.G., RAJANDREAM M.A., WALSH S.V.;

SUBMITTED (JUN-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.

-I- FUNCTION: PROBABLE AMINO-ACID OR METABOLITE TRANSPORT PROTEIN.

-I- SUBCELULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).

-I- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MANY AMINO ACID

PERMEASES.
                         UL-MAR-1989 (REL. 10, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 22, LAST ANNOTATION UPDATE)
RENA ADENINE N.6-METHYLTANSFERASE (EC 2.1.1.48) (MACROLIDE-LINCOSAMIDE-STREPTOGRAMIN B RESISTANCE PROTEIN) (ERYTHROMYCIN RESISTANCE PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 91; DB 1; Length 34v, Pred. No. 4.37e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROKARYOTA; FIRMICUTES; ACTINOMYCETALES; MYCOBACTERIACEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; A24026; A24026.
PROSITE; PS01131; RRNA_A_DIMETH; 1.
ANTIBIOTIC RESISTANCE; TRANSFERASE; METHYLTRANSFERASE.
SEQUENCE 340 Aa; 37453 MW; CE669646 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PERMEASES.
EMBL; 2740125; E248800;
PROSTIES: PS00218; AMINO ACID_PERMEASE; FALSE_NEG.
HYPOTHETICAL PROTEIN; TRANSPORT; TRANSMEMBRANE.
74 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-1996 (REL. 34, CREATED)
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
101-ULL-1998 (REL. 36, LAST ANNOTATION UPDATE)
HYPOTHETICAL 45.3 KD TRANSPORT PROTEIN CY39.19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BB359F1E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 440 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13 PSSGRPQRPVGGRSQRDRDRRVL 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44 PAAAPAGRPSASRGHRKRSRRVL 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45267 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 43.5%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WTCY39.19.
MYCOBACTERIUM TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M11276; G142204; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       440 AA;
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P09891;
01-MAR-1989 (
01-MAR-1989 (
01-NOV-1995 (
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72 RRQLPVEEPNPAKRLLFLLLTIVFCQILMAEEGVPAPLPPEDAPNAASLAPTPVSPVLEP 131
                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-S286C A. MASTON MASTON MASTON MASTALL B.G., BADCOCK K., BANKIER A.T., BOWMAN S., BROWN D., BARRELL B.G., BADCOCK K., COPSEY T., DEAR S., DEVLIN K., FRASER A., CHURCHER C.M., CONNOR R., COPSEY T., DEAR S., DEVLIN K., FRASER A., GENTLES S., HAMLYN N., HORSNELL T.S., HUNT S., JAGELS K., JONES M., LOUIS E., LYE G., MOULE S., MOULE T., ODELL C., PEARSON D., RAJANDREAM M.A., RILES L., ROWLEY N., SKELTON J., SMITH V., WALLEN C.W., WHITEHEAD S., SUBMITTED (DEC-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.

1. SIMLIARITY: BELONGS TO THE YHRO98C/YIL109C/YNL049C FAMILY. EMBL; Z47047; G762237; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 92115700.

TSAREV S.A., EMERSON S.U., REYES G.R., TSAREVA T.S., LEGTERS L.J.,
MALIK I.A., 10BAL M., PURCELL R.H.;
PROC. NATL. ACAD. SCI. U.S.A. 89:559-563(1992).

-! HEPATITIS E VIRUS IS THE MAJOR CAUSATIVE AGENT OF ENTERICALLY
TRANSMITTED NON-A, NON-B HEPATITIS (ET-NANBH).

EMBL; M80581; G329998; -
POLYPROTEIN; RNA-DIRECTED RNA POLYMERASE; HELICASE; ATP-BINDING.
NP_BIND 974 91.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1994 (REL. 28, CREATED)
01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
01-FEB-1994 (REL. 28, LAST ANNORATION UPDATE)
NON-STRUCTURAL POLYPROTEIN (CONTAINS: RNA-DIRECTED RNA POLYMERASE
(EC 2.7.7 + 8); HELLGASE).
HEPATITIS E VIRUS (STRAIN PAKISTAN) (HEV).
VIRIDAE; SS-RNA NONENVELOPED VIRUSES; CALICIVIRIDAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  729 RAATPTPAAPLPPPAPDPSPILSA-PARGEPAPGATARAPAITHQTARHRRLLF 781
                                                                                                                                                              01-FEB-1995 (REL. 31, CREATED)
01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
01-CCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
HYPOTHETICAL 103.6 KD PROTEIN IN COXSB-PFK26 INTERGENIC REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 92; DB 1; Length 926;
Pred. No. 3.34e+00;
8; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                      SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 926 AA; 103635 MW; 3F3A6839 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   114 QPMAAPAYGQPSAAMGQNMRPMNQLYPIDLLTELP 148
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                                                                                                             PRT;
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Local Similarity 45.7%;
nes 16; Conservative
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                                                                                                             STANDARD;
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HYPOTHETICAL PROTEIN
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                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                LT 43
YIK9_YEAST
P40482;
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SEQUENCE Query Match Best Loc Matches

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PROKARYOTA; FIRMICUTES; COCCI; STREPTOCOCCAEAE.
                                                                                    STRAIN-MS;
MEDLINE; 90236997.
DEMUTH D.R., GOLUB E.E., MALAMUD D.;
J. BIOL. CHEM. 265:7120-7126(1990).
                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 8.2%;
Best Local Similarity 48.6%;
Matches 17; Conservative
                STREPTOCOCCUS GORDONII.
                                                                   SEQUENCE FROM N.A.
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SIMILAR
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XX MEDLINE; 96081226.

ADRESSER D.W., HACKER A., LOVELL-BADGE R., GUERRIER D.;

LUM. MOL. GENET. 4:1613-1618(1995).

- FUNCTION: GUBUNIT OF THE STABLE BINDING OF U2 SNRNP TO THE

RASSEMBLY FORMED BY THE STABLE BINDING OF U2 SNRNP TO THE

BRANCHPOINT SEQUENCE (BPS) IN PRE-MRNA. SEQUENCE INDEPENDENT

BRANCHPOINT SEQUENCE (BPS) IN PRE-MRNA. SEQUENCE INDEPENDENT

C. ISSENTIAL, IT MAY ANCHOR U2 SNRNP TO THE PRE-MRNA.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            344 HPPAPGVHPPAPGVHPPTPGVHP-PAPGVHPPAPGVHPPA-PGVHPPPSAGVHPQAPGVH 401
                                                                                  1 MRRPLDPRDIPDELRRRLGLLDAVVIGLGSMIGAGIFAALAPAAYAAGSGLLLGLAVAAV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 HPTMTILQAPTPA-PSTIPGPRRGSGPEIFTFDPLPEPAAAPAGRPSASRGHRKRSRRVL 66
                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9; Gaps
                                                                                                                                                                                                                                                                                                                                                                                            MUS MUSCULUS (MOUSE).
EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                    .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 91; DB 1; Length 485;
Pred. No. 4.37e+00;
34; Mismatches 58; Indels
             Score 91; DB 1; Length 440;
Pred. No. 4.37e+00;
17; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                  01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SF3A66).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7E2A1448 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SSP5_STRGN STANDARD; PRT; 1500 AA. P16952; Q54184; 01-406-1990 (REL. 15, CREATED) 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE) 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE) AGGLUTININ RECEPTOR PRECURSOR.
                                                                                                                                                                                                                                                                   485 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POLY-PRO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              479 483 P
485 AA; 51279 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        124 PVSPVLEPFNLTSE-PSD 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 8.2%;
Best Local Similarity 26.8%;
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      461 PMPPMLRP-PLPSDGPGN 477
             Query Match 8.2%;
Best Local Similarity 31.1%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                SP62_MOUSE
Q62203;
                                                                                                                                                                                    129 L 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
SEQUENCE
                                                                                                                                                        61 V 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                  47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT SS AC P1 DT O1 DT DT D5 DT D5 D5 D5 D6 D6 D6 D6
                                                                                                                                                                                                                                                 RESULT
ID SF
AC Q6
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                                                                              MOC. MICROBIOL. 20:403-413(1996).

-!- FUNCTION: MAY BIND STALIC ACID RESIDUES OF SALIVARY AGGLUTININ

(SAG) IN A CALCIUM-DEPENDENT REACTION. THE INTERACTION OF SAG WITH
ITS RECEPTOR IN VARIOUS ORAL STREPTOCOCCI MODULATE BACTERIAL
COLONIZATION OF ORAL TISSUE AND IS ASSOCIATED WITH REDUCED LEVELS
                                                                                                                                                                                                                            OF DENTAL CARIES.

OF DENTAL CARIES.

DOMAIN: THE PRZ REGION, BY SIMILARITY WITH THE PROLINE RICH
DOMAINS OF THE S. PYOGENES M6 PROTEIN AND STAPHYLOCOCCAL PROTEIN A,
MAY TRAVERSE THE CELL WALL PEPTIDOGIZCAN AND IS FOLLOWED BY
HYDROPHOBIC AA WHICH MAY FUNCTION TO ANCHOR THE PROTEIN TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONSERVED IN GRAM-POSITIVE COCCI SURFACE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. CELL WALL.
-!- SIMILARITY: TO OTHER STREPTOCOCCAL AND STAPHYLOCOCCAL PROTEINS
IN THE REGION OF THE MEMBRANE ANCHOR.
-!- SIMILARITY: BELONGS TO THE SPAP/SSPS/SPAA FAMILY.
EMBL: 040026; G1100973; -.
PIR: A35186, A35186.
PROSITE: PS00343; GRAM_POS_ANCHORING; 1.
SIGNAL): REPEAT; CALCIUM-BINDING; TRANSMEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 X APPROXIMATE TANDEM REPEATS, PRI.
PRO-RICH (PR2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TO M PROTEIN OF S.PYOGÉNES.
4 X APPROXIMATE TANDEM REPEATS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRS_YEAST STANDARD; PRT; 1894 AA.
P19097;
01-NOV-1990 (REL. 16, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
FATTA ACID SYNTHASE, SUBUNIT ALPHA (EC 2.3.1.86) (CONTAINS:
EC 1.1.100, AND EC 2.3.1.41).
FASS OR YPL231W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 91; DB 1; Length 1500;
Pred. No. 4.37e+00;
4; Mismatches 13; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL. CYTOPLASMIC (POTENTIAL).
MEDLINE; 96310377.
DEMUTH D.R., DUAN Y., BROOKS W., HOLMES A.R., MCNAB
JENKINSON H.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               220 235 POTENTIAL.
301 316 POTENTIAL.
931 950 POTENTIAL.
1300 1315 POTENTIAL.
1500 AA; 164552 MW; 9361C26C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGGLUTININ RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           868 PTP-PVKIPDQPEPSKPEEPTYDPLPTPPLAPTPK 901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 PTPAPSTIPGPRRGSGPEIFTFDPLPEPAAAPAGR 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROTEINS
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1D FA

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GALLUS GALLUS (CHICKEN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AVES; NEOGNATHAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NISWANDER L., JEFFREY S., MARTIN G.R., TICKLE C.;
NATURE 371:609-612(1994).
-!- FUNCTION: MAY BE THE ENDOGENOUS RIDGE SIGNAL FOR LIMB DEVELOPMENT.
RECIPROCAL INTERACTIONS MAY CREATE A POSITIVE FEEDBACK LOOP
                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00012; PHOSPHOPANTETHEINE; 1.
PROSITE; PS00012; PHOSPHOPANTETHEINE; 1.
PROSITE; PS00012; PHOSPHOPANTETHEINE; 1.
PROSITE; PS00012; PHOSPHORANTETHEINE.
DOMAIN
POSPHOPANTETHEINE.
DOMAIN
POSPHOPANTETHEINE.
PROMAIN
POSPHOPANTETHEINE.
PHOSPHOPANTETHEINE.
PHOSPHOPANTETHEINE (BY SIMILARITY).

ACT_SITE 1312 BETA-KETOACYL SYNTHASE.
ACT_SITE 1312 BETA-KETOACYL SYNTHASE.
SCOURCE 1894 AA; 208098 MM; 310BD492 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                     MEDLINE; 94316198.
INOKOSHI J., TOMODA H., HASHIMOTO H., WATANABE A., TAKESHIMA H.,
                                        MEDLINE; 88315020.
MOHAMED A.H., CHIRALA S.S., MODY N.H., HUANG W.Y., WAKIL S.J.;
J. BIOL. CHEM. 263:12315-12325(1988).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 91; DB 1; Length 1894;
Pred. No. 4.37e+00;
13; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1996 (REL. 33, CREATED)
01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
FIBROBLAST GROWTH FACTOR-4 PRECURSOR (FGF-4) (HBGF-4).
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA: FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 36.0%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                               J03936; G171502; -.
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                                                                      [2]
MUTAGENESIS OF GLY-1257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                          PIR; A31107; A31107
SGD; L0000602; FAS2
                              SEQUENCE FROM N.A. MEDLINE; 88315020.
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P48804;
                                                                                                                             OMURA S
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